
WORLDWIDE
(TM)

Release 2.1D John F. Collins, Biocomputing Research Unit.
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Msrch_pp protein - protein database search, using Smith-Waterman algorithm
Date: Tue Mar 24 17:04:51 1998; Maspar time 3.63 Seconds
Molecular output not generated. 358,098 Million cell updates/sec

Title: >US-08-236-918A-8
Description: (1-255) From 5674704.pep
Perfect score: 1925
Sequence: 1 MGNSCYNIVATLLLVNFR.....QEDGCSGRPEEREGGCEL 255

Scoring table: PAM 150
Gap 11

Searched: 56404 seqs, 5096634 residues

Post-processing: Minimum Match 0%
Listing first 45 summaries

Database: a-issued
1:BACK1 2:51 3:52 4:53 5:54 6:55 7:56 8:57 9: PCT90
10: PCT91 11: PCT92 12: PCT93 13: PCT94 14: PCT95 15: PCT96

Statistics: Mean 30.414; Variance 146.494; scale 0.208

Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

Hit No.	Score	Query Match	Length	DB	ID	Description	Pred. No.
1	1925	100.0	255	15	PCT-US96-0	Sequence 8, Applicatio	4.99e-158
2	1925	100.0	255	7	US-08-236-	Sequence 8, Applicatio	4.99e-158
3	1116	58.0	256	7	US-08-236-	Sequence 6, Applicatio	2.44e-86
4	1116	58.0	256	15	PCT-US96-0	Sequence 2, Applicatio	2.44e-86
5	194	10.1	186	4	US-08-089-	Sequence 6, Applicatio	3.39e-07
6	183	9.5	326	5	US-08-292-	Sequence 4, Applicatio	2.46e-06
7	183	9.5	326	10	PCT-US91-0	Sequence 4, Applicatio	2.46e-06
8	174	9.0	325	10	PCT-US91-0	Sequence 2, Applicatio	1.23e-05
9	174	9.0	325	5	US-08-292-	Sequence 2, Applicatio	1.23e-05
10	163	8.5	355	5	US-08-292-	Sequence 6, Applicatio	8.63e-05
11	162	8.4	283	15	PCT-US96-1	Sequence 2, Applicatio	1.03e-04
12	140	7.3	206	5	US-08-097-	Sequence 7, Applicatio	4.69e-03
13	140	7.3	438	5	US-08-097-	Sequence 11, Applicati	4.69e-03
14	134	7.0	973	5	US-08-162-	Sequence 10, Applicati	1.30e-02
15	134	7.0	968	5	US-08-162-	Sequence 14, Applicati	1.30e-02
16	128	6.6	951	5	US-08-162-	Sequence 2, Applicatio	3.59e-02
17	127	6.6	970	14	PCT-US95-0	Sequence 11, Applicati	4.24e-02
18	123	6.4	461	1	5395760-2	Patent No. 5395760.	8.27e-02
19	123	6.4	461	7	US-08-385-	Sequence 2, Applicatio	8.27e-02
20	123	6.4	486	7	US-08-243-	Sequence 1, Applicatio	8.27e-02
21	123	6.4	518	7	US-08-385-	Sequence 4, Applicatio	8.27e-02
22	122	6.3	314	7	US-08-444-	Sequence 19, Applicati	9.76e-02

RESULT	1	ALIGNMENTS
ID	PCT-US96-03965-8	STANDARD: PRT: 255 AA.
AC	xxxxxx	
XX	01-JAN-1900	
DT	Sequence 8, Application PC/TUS9603965.	
XX		
CC	Sequence 8, Application PC/TUS9603965	
CC	GENERAL INFORMATION:	
CC	APPLICANT: Kwon, Byoung Se	
CC	APPLICANT: Kang, Chang-Yuill	
CC	TITLE OF INVENTION: Monoclonal antibody against human	
CC	NUMBER OF SEQUENCES: 10	
CC	CORRESPONDENCE ADDRESSES:	
CC	ADDRESSEE: Barnard, Brown & Michaels	
CC	STREET: 306 East State Street, Suite 220	
CC	CITY: Ithaca	
CC	STATE: NY	
CC	COUNTRY: USA	
CC	ZIP: 14850	
CC	COMPUTER READABLE FORM:	
CC	MEDIUM TYPE: Floppy disk	
CC	COMPUTER: IBM PC Compatible	
CC	OPERATING SYSTEM: PC-DOS/MS-DOS	
CC	SOFTWARE: Patentin Release #1.0, Version #1.30	
CC	CURRENT APPLICATION DATA:	
CC	APPLICATION NUMBER: PCT/US96/03965	
CC	FILING DATE:	
CC	CLASSIFICATION:	
CC	PRIOR APPLICATION DATA:	
CC	APPLICATION NUMBER: US 08/122,796	
CC	FILING DATE: 16-SEP-1993	
CC	PRIOR APPLICATION DATA:	
CC	APPLICATION NUMBER: US 08/012,269	
CC	FILING DATE: 01-FEB-1993	
CC	PRIOR APPLICATION DATA:	
CC	APPLICATION NUMBER: US 07/922,996	
CC	FILING DATE: 30-JUL-1992	
CC	PRIOR APPLICATION DATA:	
CC	APPLICATION NUMBER: US 07/267,577	
CC	FILING DATE: 07-NOV-1988	
CC	ATTORNEY/AGENT INFORMATION:	
CC	NAME: Michaels, Christopher A	

CC REGISTRATION NUMBER: 34,390
CC REFERENCE/DOCKET NUMBER: KWO5
CC TELECOMMUNICATION INFORMATION:
CC TELEPHONE: 607-273-1711
CC TELEFAX: 607-273-2609
CC INFORMATION FOR SEQ ID NO: 8:
CC SEQUENCE CHARACTERISTICS:
CC LENGTH: 255 amino acids
CC TYPE: amino acid
CC TOPOLOGY: linear
CC MOLECULE TYPE: protein
SQ SEQUENCE 255 AA: 27899 MW: 331875 CN;

Query Match 100.0%; Score 1925; DB 15; Length 255;
Best Local Similarity 100.0%; Pred. No. 4,99e-158;
Matches 255; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Db 1 MGNSCYNIVATLLVLNFERTRSLQDPCSNCPAGTFCDDNNRNQICSPCPNSFSSAGGQR 60
OY 1 MGNSCYNIVATLLVLNFERTRSLQDPCSNCPAGTFCDDNNRNQICSPCPNSFSSAGGQR 60

61 TDDICROCKGVRTRKRECSSTNAECDCPTGPHCLGAGCSMCEODCKQGOELTKKCKDC 120
OY 61 TDDICROCKGVRTRKRECSSTNAECDCPTGPHCLGAGCSMCEODCKQGOELTKKCKDC 120

121 CGTFENDQKRGICRPWTNCSLDGKSVLVNGTKERDVYCGSPADLSPGASVTPAPARE 180
OY 121 CGTFENDQKRGICRPWTNCSLDGKSVLVNGTKERDVYCGSPADLSPGASVTPAPARE 180

181 PGHSPQIISFFLALSTALFLFLFLLTFRFSVYKRGKKLLYIFKQPFMRPVQTTQEDBG 240
OY 181 PGHSPQIISFFLALSTALFLFLFLLTFRFSVYKRGKKLLYIFKQPFMRPVQTTQEDBG 240

241 CSCRPEEEEGGCEL 255
OY 241 CSCRPEEEEGGCEL 255

RESULT 2
ID US-08-236-918A-8 STANDARD; PRT: 255 AA.
AC xxxxxx
XX 01-JAN-1900
DE Sequence 8, Application US/08236918A.
XX Sequence 8, Application US/08236918A
XX Patent No. 5674704
XX GENERAL INFORMATION:
CC APPLICANT: Alderson, Mark R.
CC APPLICANT: Goodwin, Raymond G.
CC APPLICANT: Smith, Craig A.
CC TITLE OF INVENTION: Cytokine Designated 4-1BB Ligand
CC NUMBER OF SEQUENCES: 18
CC CORRESPONDENCE ADDRESS:
CC ADDRESSEE: Kathryn A. Anderson, Immunex Corporation
CC STREET: 51 University Street
CC CITY: Seattle
CC STATE: Washington
CC COUNTRY: US
CC ZIP: 98101
CC COMPUTER READABLE FORM:
CC MEDIUM TYPE: Floppy disk
CC COMPUTER: Apple Power Macintosh
CC OPERATING SYSTEM: Apple 7.5.3
CC SOFTWARE: Microsoft Word, Version #6.0.1
CC CURRENT APPLICATION DATA:
CC APPLICATION NUMBER: US/08/236,918A
CC FILING DATE: 06-May-1994
CC CLASSIFICATION: 435
CC PRIOR APPLICATION DATA:
CC APPLICATION NUMBER: US 08/060,843

CC FILING DATE: 07-May-1993
CC CLASSIFICATION: 435
CC ATTORNEY/AGENT INFORMATION:
CC NAME: Anderson, Kathryn A.
CC REGISTRATION NUMBER: 32,172
CC REFERENCE/DOCKET NUMBER: 2801-B
CC TELECOMMUNICATION INFORMATION:
CC TELEPHONE: (206) 587-0430
CC TELEFAX: (206) 233-0644
CC INFORMATION FOR SEQ ID NO: 8:
CC SEQUENCE CHARACTERISTICS:
CC LENGTH: 255 amino acids
CC TYPE: amino acid
CC TOPOLOGY: linear
CC MOLECULE TYPE: protein
SQ SEQUENCE 255 AA: 27899 MW: 331875 CN;

Query Match 100.0%; Score 1925; DB 7; Length 255;
Best Local Similarity 100.0%; Pred. No. 4,99e-158;
Matches 255; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Db 1 MGNSCYNIVATLLVLNFERTRSLQDPCSNCPAGTFCDDNNRNQICSPCPNSFSSAGGQR 60
OY 1 MGNSCYNIVATLLVLNFERTRSLQDPCSNCPAGTFCDDNNRNQICSPCPNSFSSAGGQR 60

61 TDDICROCKGVRTRKRECSSTNAECDCPTGPHCLGAGCSMCEODCKQGOELTKKCKDC 120
OY 61 TDDICROCKGVRTRKRECSSTNAECDCPTGPHCLGAGCSMCEODCKQGOELTKKCKDC 120

121 CGTFENDQKRGICRPWTNCSLDGKSVLVNGTKERDVYCGSPADLSPGASVTPAPARE 180
OY 121 CGTFENDQKRGICRPWTNCSLDGKSVLVNGTKERDVYCGSPADLSPGASVTPAPARE 180

181 PGHSPQIISFFLALSTALFLFLFLLTFRFSVYKRGKKLLYIFKQPFMRPVQTTQEDBG 240
OY 181 PGHSPQIISFFLALSTALFLFLFLLTFRFSVYKRGKKLLYIFKQPFMRPVQTTQEDBG 240

241 CSCRPEEEEGGCEL 255
OY 241 CSCRPEEEEGGCEL 255

RESULT 3
ID US-08-236-918A-6 STANDARD; PRT: 256 AA.
AC xxxxxx
XX 01-JAN-1900
DE Sequence 6, Application US/08236918A.
XX Sequence 6, Application US/08236918A
XX Patent No. 5674704
XX GENERAL INFORMATION:
CC APPLICANT: Alderson, Mark R.
CC APPLICANT: Goodwin, Raymond G.
CC APPLICANT: Smith, Craig A.
CC TITLE OF INVENTION: Cytokine Designated 4-1BB Ligand
CC NUMBER OF SEQUENCES: 18
CC CORRESPONDENCE ADDRESS:
CC ADDRESSEE: Kathryn A. Anderson, Immunex Corporation
CC STREET: 51 University Street
CC CITY: Seattle
CC STATE: Washington
CC COUNTRY: US
CC ZIP: 98101
CC COMPUTER READABLE FORM:
CC MEDIUM TYPE: Floppy disk
CC COMPUTER: Apple Power Macintosh
CC OPERATING SYSTEM: Apple 7.5.3
CC SOFTWARE: Microsoft Word, Version #6.0.1
CC CURRENT APPLICATION DATA:
CC APPLICATION NUMBER: US/08/236,918A

XX
AC xxxxxx
XX
DT 01-JAN-1900
XX
DE Sequence 6, Application US/08292549.
XX
CC Sequence 6, Application US/08292549
CC Patent No. 5464938
CC GENERAL INFORMATION:
CC APPLICANT: Smith, Craig A.
CC APPLICANT: Goodwin, Raymond G.
CC TITLE OF INVENTION: Isolated Viral Protein TNF Antagonists
CC NUMBER OF SEQUENCES: 10
CC CORRESPONDENCE ADDRESS:
CC ADDRESSEE: Immunex Corporation
CC STREET: 51 University Street
CC CITY: Seattle
CC STATE: Washington
CC COUNTRY: USA
CC ZIP: 98101
CC
CC COMPUTER READABLE FORM:
CC MEDIUM TYPE: Floppy disk
CC COMPUTER: IBM PC compatible
CC OPERATING SYSTEM: PC-DOS/MS-DOS
CC SOFTWARE: Patentin Release #1.0, Version #1.25
CC CURRENT APPLICATION DATA:
CC APPLICATION NUMBER: US/08/292,549
CC FILING DATE:
CC CLASSIFICATION: 530
CC PRIOR APPLICATION DATA:
CC APPLICATION NUMBER: 07/963,330
CC FILING DATE: 10/19/92
CC ATTORNEY/AGENT INFORMATION:
CC NAME: Perkins, Patricia A.
CC REGISTRATION NUMBER: 34,693
CC REFERENCE/DOCKET NUMBER: 2602-A
CC TELECOMMUNICATION INFORMATION:
CC TELEPHONE: (206) 587-0430
CC TELEFAX: (206) 233-0644
CC INFORMATION FOR SEQ ID NO: 6:
CC SEQUENCE CHARACTERISTICS:
CC LENGTH: 355 amino acids
CC TYPE: amino acid
CC TOPOLOGY: linear
CC MOLECULE TYPE: Protein
CC SEQUENCE 355 AA; 39008 MW; 711992 CN;
SQ
Query Match 8.5%; Score 163; DB 5; Length 355;
Best Local Similarity 34.9%; Pred. No. 8.63e-05;
Matches 30; Conservative 21; Mismatches 24; Indels 11; Gaps 8;
DB 42 CLSCPGTVA SRLDSTNTNTOCTPCASDFTSRNNHLPACISGNGRCDSDNVERPSCN 101
XX
DT 01-JAN-1900
XX
DE Sequence 2, Application PC/TUS9612374.
XX
CC Sequence 2, Application PC/TUS9612374
CC GENERAL INFORMATION:
CC APPLICANT: Northwestern University
CC

CC
CC TITLE OF INVENTION: Herpes Virus Entry Mediator
CC NUMBER OF SEQUENCES: 5
CC CORRESPONDENCE ADDRESS:
CC ADDRESSEE: Dressler, Goldsmith, Milnamow & Katz, Ltd.
CC STREET: 180 N. Stetson, Suite 4700
CC CITY: Chicago
CC STATE: Illinois
CC COUNTRY: U.S.A.
CC ZIP: 60601
CC
CC COMPUTER READABLE FORM:
CC MEDIUM TYPE: Floppy disk
CC COMPUTER: IBM PC compatible
CC OPERATING SYSTEM: PC-DOS/MS-DOS
CC SOFTWARE: Patentin Release #1.0, Version #1.30
CC CURRENT APPLICATION DATA:
CC APPLICATION NUMBER: PCT/US96/12374
CC FILING DATE:
CC CLASSIFICATION:
CC ATTORNEY/AGENT INFORMATION:
CC NAME: Northrup, Thomas E.
CC REGISTRATION NUMBER: 33,268
CC REFERENCE/DOCKET NUMBER: NOR3446P020PC
CC TELECOMMUNICATION INFORMATION:
CC TELEPHONE: (312) 616-5400
CC TELEFAX: (312) 616-5460
CC
CC INFORMATION FOR SEQ ID NO: 2:
CC SEQUENCE CHARACTERISTICS:
CC LENGTH: 283 amino acids
CC TYPE: amino acid
CC TOPOLOGY: linear
CC MOLECULE TYPE: Protein
CC SEQUENCE 283 AA; 30519 MW; 429998 CN;
SQ
Query Match 8.4%; Score 162; DB 15; Length 283;
Best Local Similarity 30.7%; Pred. No. 1.03e-04;
Matches 23; Conservative 16; Mismatches 32; Indels 4; Gaps 4;
DB 67 CGELGTVCPEPCPPGYIAHLNLSKLCQCDMPAGLRATNCRSTENAVGCCSPGFH 126
XX
DT 01-JAN-1900
XX
DE Sequence 7, Application US/08097827.
XX
CC Sequence 7, Application US/08097827
CC Patent No. 5457035
CC GENERAL INFORMATION:
CC APPLICANT: Baum, Peter
CC APPLICANT: Goodwin, Ray
CC APPLICANT: Penslow, William
CC APPLICANT: Gayle, Richard
CC TITLE OF INVENTION: No. 5457035el Cytokine which is a ligand for
CC NUMBER OF SEQUENCES: 13
CC CORRESPONDENCE ADDRESS:
CC ADDRESSEE: Immunex Corporation
CC STREET: 51 University Street
CC CITY: Seattle
CC STATE: WA
CC COUNTRY: USA
CC ZIP: 98101
CC

CC INFORMATION FOR SEQ ID NO: 10:
CC SEQUENCE CHARACTERISTICS:
CC LENGTH: 973 amino acids
CC TYPE: amino acid
CC TOPOLOGY: linear
CC MOLECULE TYPE: protein
SQ SEQUENCE 973 AA; 107980 MW; 4944642 CN;

Query Match 7.0%; Score 134; DB 5; Length 973;
Best Local Similarity 35.7%; Pred. No. 1.30e-02;
Matches 25; Conservative 15; Mismatches 23; Indels 7; Gaps 5;

Db 250 AMKDTQCACGPGTFFKSKQEGPCPPNSRTTAGATVC-ICR--SGFFRA--D-ADP 303
QY 23 SLDDP-CSNCPACTFCDNNRNOICSPCPNFSAGQRTCDICRCKGVFRTKRCSSST 81

Db 304 ADSACTSVPS 313
QY 82 SNAECDCTPG 91

IT 15
ID US-08-162-809-14 STANDARD; PRT; 988 AA.

AC xxxxxx

DT 01-JAN-1900

DE Sequence 14, Application US/08162809.

CC Sequence 14, Application US/08162809

CC Patent No. 5457048

CC GENERAL INFORMATION:

CC APPLICANT: Pasquale, Elena B.

CC TITLE OF INVENTION: NOVEL EPH-RELATED TYROSINE KINASES,

CC TITLE OF INVENTION: NUCLEOTIDE SEQUENCES, AND METHODS OF USE

CC NUMBER OF SEQUENCES: 26

CC CORRESPONDENCE ADDRESS:

CC ADDRESSEE: CAMPBELL AND FLORES

CC STREET: 4370 La Jolla Village Drive, Suite 700

CC CITY: San Diego

CC STATE: California

CC COUNTRY: United States of America

CC ZIP: 92122

CC COMPUTER READABLE FORM:

CC MEDIUM TYPE: floppy disk

CC OPERATING SYSTEM: PC-DOS/MS-DOS

CC SOFTWARE: Patent Release #1.0, Version #1.25

CC CURRENT APPLICATION DATA:

CC APPLICATION NUMBER: US/08/162,809

CC FILING DATE:

CC CLASSIFICATION: 514

CC ATTORNEY/AGENT INFORMATION:

CC NAME: Campbell, Cathryn A.

CC REGISTRATION NUMBER: 31,815

CC TELECOMMUNICATION INFORMATION:

CC TELEPHONE: (619) 535-9001

CC TELEFAX: (619) 535-8949

CC INFORMATION FOR SEQ ID NO: 14:

CC SEQUENCE CHARACTERISTICS:

CC LENGTH: 988 amino acids

CC TYPE: amino acid

CC TOPOLOGY: linear

CC MOLECULE TYPE: protein

SQ SEQUENCE 988 AA; 109578 MW; 5106875 CN;

Db 250 AMKDTQCACGPGTFFKSKQEGPCPPNSRTTAGATVC-ICR--SGFFRA--D-ADP 303
QY 23 SLDDP-CSNCPACTFCDNNRNOICSPCPNFSAGQRTCDICRCKGVFRTKRCSSST 81
Db 304 ADSACTSVPS 313
QY 82 SNAECDCTPG 91

Search completed: Tue Mar 24 17:05:21 1998
Job time : 30 secs.

Query Match 7.0%; Score 134; DB 5; Length 988;
Best Local Similarity 35.7%; Pred. No. 1.30e-02;
Matches 25; Conservative 15; Mismatches 23; Indels 7; Gaps 5;

Db 181 pghspqisfflaltstallflfflltrfsvvkrgrklllyfkqpfmrpvqtgeedg 240
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Qy 181 PGHSQIISFFLALTSTALLFLFLTRFSVVKRGKRLKLIIFKQPFMRPVQTGEEDG 240
Db 241 cscrfeeeggccl 255
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Qy 241 CSCRPEEEEGGCEL 255

RESULT 2
ID R70977 standard; Protein; 255 AA.
AC R70977;
DT 16-OC7-1995 (first entry)
DE H4-1BB receptor protein.
KW H4-1BB; receptor protein; immunosuppressive; autoimmune disease;
OS Homo sapiens.
PN WO9507984-A.
PD 23-MAR-1995.
P 15-SEP-1994; U10457.
P 16-SEP-1993; US-122796.
I (INDV) UNITV INDIANA FOUND.
PI Kwon BS;
DR WPI: 95-131352/17.
DR N-PSDB; 086126.
PT Novel cDNA encoding human receptor protein H4-1BB - useful to
PT produce the protein which is used to treat auto-immune disease
PT and facilitate organ transplantation
PS Claim 6; Fig.2; 36pp; English.
CC Human peripheral blood lymphocyte-derived cDNA was amplified by PCR
CC using probes based on the mouse receptor protein 4-1BB gene. The PCR
CC product was used to screen a cDNA library of activated human T-cells.
CC The isolated cDNA (086126), deposited as NRRL B21131, encoded the
CC human homolog, H4-1BB (R70977), of 4-1BB.
SQ Sequence 255 AA;

Query Match 100.0%; Score 1925; DB 13; Length 255;
Best Local Similarity 100.0%; Pred. No.7,29e-167;
Matches 253; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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Db 61 tcdicrckgyvfrtrkccsstnaecdctpgfhclgagcmcegdckqgqeltkkqcdc 120
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Db 121 cffgtndgkrigicrptwncslqgksvlyngtkerdvvcgspadispasvtpapare 180
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Qy 121 CFFGTNDGKRIGICRPTWNCSLQGKSVLYNGTKERDVVCGPSADISPGASVTPAPARE 180
Db 181 pghspqisfflaltstallflfflltrfsvvkrgrklllyfkqpfmrpvqtgeedg 240
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Qy 181 PGHSQIISFFLALTSTALLFLFLTRFSVVKRGKRLKLIIFKQPFMRPVQTGEEDG 240
Db 241 cscrfeeeggccl 255
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Qy 241 CSCRPEEEEGGCEL 255

RESULT 3
ID W04174 standard; Protein; 255 AA.
AC W04174;
DT 12-DEC-1996 (first entry)
DE Human receptor H4-1BB.
KW Receptor 4-1BB; H4-1BB; monoclonal antibody; T-lymphocyte; T-cell;
KW B-lymphocyte; B-cell; immunostimulant; cancer; autoimmune disease;
KW graft rejection; therapy.
OS Homo sapiens.
PN WO9629348-A1.
PD 26-SEP-1996.

PF 22-MAR-1996; U03965.
PR 23-MAR-1995; US-409851.
PA (INDV) UNITV INDIANA FOUND.
PI Kang C, Kwon BS;
DR WPI: 96-443138/44.
DR N-PSDB; T39546.
PT Monoclonal antibody specific for human receptor protein 4-1BB - used
PT to enhance proliferation and activation of T-cells for treatment of
PT cancer and to inhibit specific ligand binding for treating
PT auto-immune diseases
PS Disclosure; Page 36-37; 48pp; English.
CC Novel human receptor protein H4-1BB (W04174) has the potential to
CC function as an accessory signaling molecule during T-cell activation
CC and proliferation. Its amino acid sequence was deduced from a cDNA
CC clone (T39546) isolated from activated human T-lymphocytes.
CC Recombinant H4-1BB can be produced in transfected host cells. It is
CC used to isolate receptor ligands, to stimulate B-cells expressing such
CC ligands and to block H4-1BB ligand binding. A fusion protein of
CC H4-1BB with human placental alkaline phosphatase can be used to modify
CC immune responses. A monoclonal antibody raised against an
CC immunopeptide (see also W04172) of H4-1BB is useful in the treatment
CC of cancer and autoimmune diseases.
SQ Sequence 255 AA;

Query Match 98.5%; Score 1897; DB 18; Length 255;
Best Local Similarity 99.6%; Pred. No.3,21e-164;
Matches 254; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Db 1 mgnsynvatalllvlnfertrslqpcsnpcagtfcdnurnqicpcppnsfssagqr 60
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Qy 1 MGNSYNVATALLVLNFERTRSLQDPCSNCPAGTFCDNURNQICPCPPNFSFSSAGQR 60
Db 61 tcdicrckgyvfrtrkccsstnaecdctpgfhclgagcmcegdckqgqeltkkqcdc 120
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Qy 61 TCDICRCKGYVFRTRKCCSSTNAECDCTPGFHCLGAGCSMCEODCKQGOELTKKGCDC 120
Db 121 cffgtndgkrigicrptwncslqgksvlyngtkerdvvcgspadispasvtpapare 180
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Qy 121 CFFGTNDGKRIGICRPTWNCSLQGKSVLYNGTKERDVVCGPSADISPGASVTPAPARE 180
Db 181 pghspqisfflaltstallflfflltrfsvvkrgrklllyfkqpfmrpvqtgeedg 240
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Qy 181 PGHSQIISFFLALTSTALLFLFLTRFSVVKRGKRLKLIIFKQPFMRPVQTGEEDG 240
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|||
Qy 241 CSCRPEEEEGGCEL 255

RESULT 4
ID R74087 standard; Protein; 255 AA.
AC R74087;
DT 21-JAN-1996 (first entry)
DE Human receptor induced by lymphocyte activation (IIA).
KW IIA: receptor inducible by lymphocyte activation; disease diagnosis;
KW antiinflammatory.
OS Homo sapiens.
FH Key Location/Qualifiers
FT Peptide 1..17
FT /note- "signal peptide"
FT Domain 187..213
FT /note- "transmembrane domain"
FT MISC_difference 138
FT /note- "potential N-glycosylation site"
FT MISC_difference 149
FT /note- "potential N-glycosylation site"
FT MISC_difference 242
FT /note- "protein-kinase phosphorylation site"
FT MISC_difference 234
FT /note- "casein-kinase-II phosphorylation site"
FT MISC_difference 235
FT /note- "casein-kinase-II phosphorylation site"
FT Binding_site 241..244

/note- "potential ligand binding site"

CA2108401-A.
 28-MAR-1995.
 14-OCT-1993; 108401.
 27-SEP-1993; US-127693.
 (REGC) UNIV CALIFORNIA.
 PI Lotz M, Schwarz H;
 DR WPI: 95-194420/26.
 DR N-PSDB; R74087.
 New receptor inducible by lymphocyte activation - used to develop
 PT prods. for the diagnosis and treatment of inflammatory host defence
 pathology.
 PS Claim 55: Page 61; 91pp; English.
 CC ILA may be used to identify a host defence inflammatory response in
 CC body tissue. The ILA agent can be used to detect an ILA-mediated
 CC pathology such as atherosclerosis, autoimmune disease (rheumatoid
 CC arthritis), transplant rejection, pathogenic host defense responses
 CC to microorganism and malignancy such as lung carcinoma.
 SQ Sequence 255 AA;

Query Match 97.2%; Score 1871; DB 13; Length 255;
 Best Local Similarity 98.4%; Pred. No. 9,136-162;
 Matches 251; Conservative 2; Mismatches 2; Indels 0; Gaps 0;

Db 1 mgncynvavtllvllvntertrslqpcsnpcatfcdntrngicpcpmsfssagqr 60
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 QY 1 MGNSCYNVAVTLLVLFNFRTRSLQPCSNPCATFCDDNNRQICSPCPMSFSSAGQR 60

Db 61 tcdlwrqgkyftrfkrkccstsnaccdtpgfqvlagacsmcbedckogdeltkkgckdc 120
 |||||
 QY 61 TCDICROCKGVFRFRKCCSTSNACCDTPGFHCLGACSMCEBCKOGDELTKKGCKDC 120

Db 121 cftgfndqkrgicrptncslqgksvlnqtkerdvvcgspadlspassvtpapare 180
 |||||
 QY 121 CFGFNDQKRGICRPTNCSLDGKSVLVNQTKEKRDVVCSPADLSPASSVTPAPARE 180

Db 181 pghspqllsfflaltstalllflfltrfsvkrklllyfkqfmrpvqtqeedg 240
 |||||
 QY 181 PGHSPQILSFFLALTSTALLFLFLTRFSVYKRGKRLLYFKQPMRPVQTQEEEDG 240

Db 241 cscrfeeeggecel 255
 |||||
 QY 241 CSCRPEEGBGCEL 255

RESULT 5
 ID W04173 standard; Protein; 256 AA.
 12-DEC-1996 (first entry)
 Mouse receptor 4-1BB.
 KW Receptor 4-1BB; H4-1BB; monoclonal antibody; T-lymphocyte; T-cell;
 KW immunostimulant; cancer; autoimmune disease; graft rejection;
 KW therapy.
 OS Mus SP.
 PN W03623348-A1.
 PD 26-SEP-1996.
 PF 22-MAR-1996; U03965.
 PR 23-MAR-1995; US-409851.
 PA (INDV) UNIV INDIANA FOUND.
 PI Kang C, Kwon BS;
 DR WPI: 96-443138/44.
 DR N-PSDB; T39541.
 PT Monoclonal antibody specific for human receptor protein 4-1BB - used
 PT to enhance proliferation and activation of T-cells for treatment of
 PT cancer and to inhibit specific ligand binding for treating
 PT auto-immune diseases
 PS Disclosure; Page 32-34; 48pp; English.
 CC Novel murine receptor protein 4-1BB (W04173) has the potential to
 CC function as an accessory signaling molecule during T-cell activation
 CC and proliferation. It may represent a cell surface molecule
 CC involved in T-cell/APC interactions and may also act as a B-cell
 CC costimulator. It is structurally related to members of the nerve
 CC growth factor receptor superfamily. Its amino acid sequence was

CC deduced from an isolated cDNA clone (see also T39541). A human
 CC homologue, H4-1BB (W04174), was identified and used to raise a
 CC monoclonal antibody useful in cancer and autoimmune disease therapy.
 SQ Sequence 256 AA;

Query Match 58.0%; Score 1116; DB 19; Length 256;
 Best Local Similarity 57.3%; Pred. No. 8,276-91;
 Matches 145; Conservative 49; Mismatches 55; Indels 4; Gaps 4;

Db 1 mgncynvavtllvllvntertrslqpcsnpcatfcdntrngicpcpmsfssagqr 59
 |||||
 QY 1 MGNSCYNVAVTLLVLFNFRTRSLQPCSNPCATFCDDNNRQICSPCPMSFSSAGQR 60

Db 60 ncnicrcaagyftrfkrkccstsnaccdtpgfqvlagacsmcbedckogdeltkkgckdc 119
 |||||
 QY 61 TCDICROCKGVFRFRKCCSTSNACCDTPGFHCLGACSMCEBCKOGDELTKKGCKDC 120

Db 120 slgftndqngtvcprptncslqgksvlnqtkerdvvcgspadlspassvtpapare 179
 |||||
 QY 121 CFGFNDQKRGICRPTNCSLDGKSVLVNQTKEKRDVVCSPADLSPASSVTPAPARE 179

Db 180 g-gnslqvltrftrfkrkccstsnaccdtpgfqvlagacsmcbedckogdeltkkgckdc 237
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 QY 180 EPGHSPQILSFFLALTSTALLFLFLTRFSVYKRGKRLLYFKQPMRPVQTQEEEDG 239

Db 238 aacscrpeeggeeg 250
 |||||
 QY 240 GCSRPEEGBGCEL 252

RESULT 6
 ID R64199 standard; Protein; 256 AA.
 AC R64199;
 DT 08-AUG-1995 (first entry)
 DE Murine 4-1BB polypeptide.
 KW T-cell; lymphocyte; activation; tissue culture; clone; cell lines;
 KW proliferation; stimulation; 4-1BB-L; ligand; receptor; cytokine.
 OS Mus musculus.
 PN W03426290-A.
 PD 24-NOV-1994.
 PF 06-MAY-1994; U05036.
 PR 07-MAY-1993; US-060843.
 PA (IMMUNEX) IMMUNEX CORP.
 PI Alderson MR, Goodwin RG, Smith CA;
 DR WPI: 95-022265/03.
 DR N-PSDB; Q75428.
 PT Cytokine, 4-1BB ligand (4-1BB-L) - binds to cell surface receptor
 PT 4-1BB to transduce signal
 PS Example 1; Page 44-45; 65pp; English.
 CC The 4-1BB polypeptide (receptor) and the 4-1BB-L (cytokine, see
 CC Q75422) are useful in a pharmaceutical composition for stimulating
 CC the immune system. The 4-1BB and 4-1BB-L polypeptides are also useful
 CC for exploring mechanisms of T-cell activation, as they are expressed
 CC on T lymphocytes. 4-1BB-L can be used as a tissue culture reagent for
 CC in vitro cultivation of primary T-cells during the derivation of
 CC clonal T-cell lines. It may also be used to stimulate proliferation
 CC of activated T-cells, used in therapeutic procedures.
 SQ Sequence 256 AA;

Query Match 58.0%; Score 1116; DB 12; Length 256;
 Best Local Similarity 57.3%; Pred. No. 8,276-91;
 Matches 145; Conservative 49; Mismatches 55; Indels 4; Gaps 4;

Db 1 mgncynvavtllvllvntertrslqpcsnpcatfcdntrngicpcpmsfssagqr 59
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 QY 1 MGNSCYNVAVTLLVLFNFRTRSLQPCSNPCATFCDDNNRQICSPCPMSFSSAGQR 60

Db 60 ncnicrcaagyftrfkrkccstsnaccdtpgfqvlagacsmcbedckogdeltkkgckdc 119
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 QY 61 TCDICROCKGVFRFRKCCSTSNACCDTPGFHCLGACSMCEBCKOGDELTKKGCKDC 120

Db 120 slgftndqngtvcprptncslqgksvlnqtkerdvvcgspadlspassvtpapare 179
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 QY 121 CFGFNDQKRGICRPTNCSLDGKSVLVNQTKEKRDVVCSPADLSPASSVTPAPARE 179

Db 180 g-gnslqvltrftrfkrkccstsnaccdtpgfqvlagacsmcbedckogdeltkkgckdc 237
 |||||
 QY 180 EPGHSPQILSFFLALTSTALLFLFLTRFSVYKRGKRLLYFKQPMRPVQTQEEEDG 239

Db 238 aacscrpeeggeeg 250
 |||||
 QY 240 GCSRPEEGBGCEL 252

```

OY 121 CFTGFNDOK-RGICRPMTNCSLDGKSVLVNGTKERDVYCGSPADLSPGASSVTPAPAR 179
Db 180 g-ghslyvltlflalts-allaifitlllsyvkwtktkphlftkqpfktttaageed 237
OY 180 EPGHSPDISEFLLTSTALLFLFFLTLRSSVYKRGKRLLTYFKOPFMKPVOTQED 239
Db 238 acscrcpgeeg 250
OY 240 GCSCRFPBEEBGG 252

RESULT 7
ID R70978 standard; Protein; 256 AA.
AC R70978;
DE 16-OCT-1995 (first entry)
DE 4-1BB receptor protein.
KW 4-1BB; receptor protein; immunosuppressive; autoimmune disease;
OS organ transplantation; cell membrane ligand.
FH Key Location/Qualifiers
FT Peptide 1..23
FT /label= sig_peptide
PD WO9507984-A.
PE 23-MAR-1995.
PR 15-SEP-1994; US-10457.
PR 16-SEP-1993; US-122796.
PA (INDV) UNIT INDIANA FOUND.
PI Kwon BS;
DR WPI; 95-131352/17.
DR N-PSDB; 086127.
PT Novel cDNA encoding human receptor protein H4-1BB - useful to
PT produce the protein which is used to treat auto-immune disease
PT and facilitate organ transplantation
PS Disclosure; Fig.1; 36pp; English.
CC cDNA encoding the human receptor protein H4-1BB (given in Q86126)
CC was isolated using PCR primers based on the homologous mouse
CC 4-1BB gene (Q86127) encoding mouse receptor protein (R70978).
SQ Sequence 256 AA;

Query Match 58.0%; Score 1116; DB 13; Length 256;
Best Local Similarity 57.3%; Pred. No. 8.27e-91;
Matches 145; Conservative 49; Mismatches 55; Indels 4; Gaps 4;

Db 1 mgmcyvvvvlvlllygckvgavnsdncqpfctky-nyvckspstfsslgqp 59
OY 1 MGNCYNIVATLLVLENERTRSLQDPCSNCPAGTFCDDNNNOICSPCPNPSFSSAGQR 60
Db 60 ncnicrvacyffrkfkfscsthaeccciefhclpqcctcekdcrpgeitkgqctc 119
61 TCDCRCCKGVFRTRKESSTSNABCDCTPFCFLGAGCSMCBDDCKGQELTKKCKDC 120
Db 120 slgtfndqngtgcrcpwtncslldgrsvlktgltedvvcgppvvvsfsspttltvpeggp 179
OY 121 CFTGFNDOK-RGICRPMTNCSLDGKSVLVNGTKERDVYCGSPADLSPGASSVTPAPAR 179
Db 180 g-ghslyvltlflalts-allaifitlllsyvkwtktkphlftkqpfktttaageed 237
OY 180 EPGHSPDISEFLLTSTALLFLFFLTLRSSVYKRGKRLLTYFKOPFMKPVOTQED 239
Db 238 acscrcpgeeg 250
OY 240 GCSCRFPBEEBGG 252

```

```

FT Peptide 1..20
FT /label= signal
FT Protein 21..260
FT /label= CD27_antigen
FT Domain 21..191
FT /label= extracellular
FT Region 192..211
FT /label= transmembrane
FT Domain 212..260
FT /label= cytoplasmic
PD WO9201049-A.
PE 23-JAN-1992.
PR 15-JUL-1990; US-04986.
PR 13-JUL-1990; US-553759.
PA (GENE) GEN HOSPITAL CORP.
PI Seed B, Aruifo A, Amlot M;
DR WPI; 92-056864/07.
DR N-PSDB; 021183.
PT New CD53 cell surface antigen and DNA encoding it - for
PT immuno-therapy and diagnosis of haematopoietic neoplasms, etc.
PS Example 13; Page 103; 160pp; English.
CC The amino acid sequence of CD27 was deduced from a cDNA clone
CC obtained from human T lymphocyte cDNA transferred into COS cells
CC and immunoselected using the Mabs OKT18a and CLB-9f4 (see e.g.
CC Q21164 for description of the rapid immunoselection cloning method).
CC The CD27 polypeptide demonstrates the typical features of a type I
CC integral membrane protein. The hydrophobic membrane spanning region
CC is followed by a cytoplasmic domain beginning with a positively
CC charged stop transfer sequence. The deduced CD27 sequence is highly
CC homologous to the B lymphocyte and carcinoma antigen CD40 over its
CC entire length. CD27 is also homologous to the NRP receptor over the
CC extracellular and transmembrane domains. There is a cysteine and
CC histidine-rich region in the extracellular domain which could
CC potentially form "zinc fingers", followed by a serine, threonine
CC and proline rich membrane proximal domain.
SQ Sequence 260 AA;

Query Match 10.3%; Score 199; DB 4; Length 260;
Best Local Similarity 38.6%; Pred. No. 1.58e-07;
Matches 27; Conservative 14; Mismatches 25; Indels 4; Gaps 4;

Db 53 cdghrkaagcdpdpysfspdhtphrcscrhnsqglivrr-cltlaaeacrrng 111
OY 37 CDNNRNRIR-CSPCPN-SFSSAGQR-CDICRCCKGVFRTRKESSTSNABCDCTPFGH 93
Db 112 crckctecd 121
OY 94 CLGAGCMCE 103

RESULT 9
ID R91441 standard; Protein; 260 AA.
AC R91441;
DE 31-OCT-1996 (first entry)
DE Human CD27 antigen
KW Cell surface antigen; cloning; immunoselection; immunotherapy;
KW therapy; diagnosis; vector; CD27 antigen; T-Lymphocyte;
KW autoimmune disease.
OS Homo sapiens.
FH Key Location/Qualifiers
FT Peptide 1..20
FT /label= sig_peptide
FT Domain 21..91
FT /label= Extracellular_domain
FT Domain 92..212
FT /label= Transmembrane_domain
FT Domain 213..260
FT /label= Cytoplasmic_domain
PD US5506126-A.
PE 09-APR-1996.
PR 25-FEB-1988; 160416.
PR 25-FEB-1988; US-160416.
PR 13-JUL-1989; US-379076.

```


Query Match 9.5%; Score 103; DB 5; Length 326;
Best Local Similarity 31.5%; Pred. No. 3,266-06;
Matches 28; Conservative 20; Mismatches 32; Indels 9; Gaps 5

Dd 40 ctscpgsyasrlcgpasdvctscpknetflastnhapacvscrgtghlssesqcdkt 99
:::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|
Oy 28 CSNCDVGFTE---CDNNRNQICSPCPNFSSAGGQ-RITDCIDR-QCKGVFRTTRKESST 81

Dd 100 rdvrccsaagnycllkxgqecrclcapqtk 128
:||||:|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|
Oy 82 SNAECDCTPFHCLT--G-AGCSMCEDOCK 107

RESULT 13

ID R85071 standard; Protein; 325 AA.
AC R85071;
DT 16-APR-1996 (first entry)
DE Shope fibroma virus T2 protein.
KW Shope fibroma virus; rabbit fibroma virus; immunosuppressive;
KW cytokine antagonist; tumour necrosis factor antagonist;
KW therapeutic; cachexia; septic shock.
DB Rabbit fibroma virus.
UNOSUS464938-A.
PD 07-NOV-1995.
PE 18-AUG-1994; 292549.
PR 19-OCT-1992; US-963330.
PA (IMMV) Immunex Corp.
PI Goodwin RG, Smith CA
PWJ: 95-402861/51.
DR N-PSDS: T02470.

PT New soluble viral proteins that bind tumour necrosis factor - for treating cachexia, septic shock, side effects of TNF therapy etc., also useful in assays, affinity purification, and antibody prodn.
PS Claim 1; Columns 25-28; 21pp; English.
CC The Shope fibroma virus T2 protein is a soluble viral protein which binds tumour necrosis factor (TNF), thus inhibiting TNF binding to its receptor. T2 protein is useful (when administered by injection or infusion from sustained release implants, etc.) for treating TNF associated toxicity e.g. side effects of using TNF as an antitumour agent or in cases of cachexia and septic shock where TNF production is excessive.
SO Sequence 325 AA;

Query Match 9.0%; Score 174; DB 15; Length 325;
Best Local Similarity 31.3%; Pred. No. 1,756-05;
Matches 25; Conservative 15; Mismatches 35; Indels 5; Gaps 4;

Dd 49 asrlcgpsntvcspcedgfitaashnapavscrgptghlssesqpdrhdrcvncst 108
:::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|
33 AGTFDDNRNKQICSPCPNFSSAGGQ-RITDCIDR-QCKGVFRTTRKESSTYNAECDCTP 90

Dd 109 gnycollkgagncrclcapqtk 128
|||::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|
Oy 91 GFHCLT-G-AGCSMCEDOCK 107

RESULT 14

ID R27865 standard; Protein; 325 AA.
AC R27865;
DT 11-MAR-1993 (first entry)
DE Rabbit fibroma virus T2 protein.
KW Polymerase chain reaction; TNF antagonist; tumour necrosis factor.
DB Rabbit fibroma virus.
UNW09217583-A.
PN 15-OCT-1992.
PE 29-MAR-1991; U02207.
PR 29-MAR-1991; WO-U22076.
PA (IMMV) IMMUNEX CORP.
PI Goodwin RG, Smith CA.
PWJ: 92-366255/44.
DR N-PSDS: Q29744.

PT Isolated viral proteins are cytokine (e.g. TNF) antagonists - for regulating immune response and for treating cachexia septic shock

[illegible]

Db 253 gaagcgcgaacttaacatcgcagagtgctgcgcgactattcaagttcaagaagcttt 312
 |||||
 QY 292 GACAAAGACCTGTGACATATGAGGCACTGTAAAGGGTTTTCAGGACCGAGAACGT 351
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 Db 313 gctcctctaccacacgcgcgagcttgagtgattgaagagattccattgctctg9ggccac 372
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 QY 352 GTTCTCTCCACCACTATGACAGAGTGTGACTGTCACTCCAGGGTTTCTACTGCTGGGGCAG 411
 |||||
 Db 373 agtgcacagatgtlgaagagagactcgaagctcgcgcgcaggaagctaacgaagcag9gttc 432
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 QY 412 GATGACAGCATGTGTGANAAGATTGTAAACAGAGTCAGAA - CTGACAAAAAAGGTGT 470
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 Db 433 aaaaactgtagcttgcggaaacattaaatgcacgaacgcggagagtgctctgcacccctgg 492
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 QY 471 AAAGACCTGTGCTTGGGACATTTAAACGATCAGAAAGCT - GGCAAT - CTGTGACCCCTGA 528
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 Db 493 cgcgggctgcatactcattatgctctgtcctaa - gaccgcggaacacgcggagaagaagctgg 551
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 Db 529 CAAACTTTCTTTGGATGGAAGCTGTCTCTTTGTAATGGGACGAAGAGAGGACACTGG 588
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 QY 589 TCTGTGGACC 598
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RESULT	3				
LOCUS	R06117	278 bp	mRNA	EST	03-APR-1995
DEFINITION	ye9b09.s1 Homo sapiens cDNA clone 124889 3'			similar to	containing
	Alu repetitive element.				

ACCESSION	R0611/
NID	9756737
KEYWORDS	EST.

SOURCE human clone-124889 library-Souares fetal liver spleen hNFs (pMTT3D (Pharmacia) with a modified polylinker hNFs-DH10B (ampicillin resistant) primer-2mls RstlelPac I Rstle2-Eco RI Liver and spleen from a 20 week-post conception male fetus. 1st strand cDNA was primed with a Pac I - oligo(dT) primer [5', ACTCGACAGATTAATTAAGAATCTTTTTTTTTTTTTTTT 3'], double-stranded cDNA was ligated to Eco RI adaptors (Pharmacia), digested with Pac I and cloned into the Pac I and Eco RI sites of the modified pMTT3 vector. Library went through one round of normalization. Library constructed by Bento Soares and M.Fatima Bonalato.

ORGANISM	REFERENCE
Homo sapiens	1 (Bases 1 to 278)
Eucaryotes	1 (Bases 1 to 278)
Metazoa	1 (Bases 1 to 278)
Chordata	1 (Bases 1 to 278)
Vertebrata	1 (Bases 1 to 278)
Gnathostomata	1 (Bases 1 to 278)
Eutheria	1 (Bases 1 to 278)
Primates	1 (Bases 1 to 278)
Catarrhini	1 (Bases 1 to 278)
Hominidae	1 (Bases 1 to 278)
Homo	1 (Bases 1 to 278)

AUTHORS
Hallier, L., Clark, N., Dubuque, T., Elliston, K., Hawkins, M.,
Holman, M., Hultman, M., Kucaba, T., Le M., Lennon, G., Marris, M.,
Patterson, J., Rifkin, U., Rohlfing, T., Soares, M., Tan, F.,
Trevaskis, E., Waterston, R., Williamson, A., Wohldmann, P. and
Wilson, R.

TITLE
The Mashu-Merck EST Project

JOURNAL
Unpublished (1995)

COMMENT
Contact: Wilson, R.

CONTACT: WALSON RA
 MasNú-Merck EST Project
 Washington University School of Medicine
 4444 Forest Park Parkway, Box 850L, St. Louis, MO 63108
 Tel: 314 286 1800
 Fax: 314 286 1810
 Email: estewatson.wustl.edu
 High quality sequence stops: 257
 Source: IMAGE Consortium, LNL
 This clone is available royalty-free through LNL ; contact the
 IMAGE Consortium (info@image.lnl.gov) for further information.
 Location/Qualifiers

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source 1..278 /organism="Homo sapiens"
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	/clone="124889"			
BASE COUNT	85 a	60 c	76 g	56 t
ORIGIN				1 others

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	Matches 188;	Conservative 0;	Mismatches 50; Indels 2; Gaps 2.
Db	41	ggaggaattacttgagcttgagagtttgagaccagcctcgtggcaacatgccaaccccatg	100
Cp	1305	ggagggcccaaaGTGAACCTAGAGAGTTTGAGACCAACCCGTGTACAATGGCAAAAGCCATC	1246
Db	101	tttccaaaa-aaaaaatacaaaaattgctggtgtgtgtgtgtagctgctgtagctccag	159
Cp	1245	TTTTACCAAAACAAAAAACAAAAATTGTAGTCAGGTGTGTGGCCCTTCTCTGTATTCTTCAG	1186
Db	160	ctatggagagcctgtagtgtgggagagataccctgaac-ccagaggtctgaagctgcagcgaa	218
Cp	1185	CTACTAGAGAGCTAGAGGAGAGAGGATCACTTGTAGCTCCCAAGGTCCAAGGCTGCAGAGAG	1126
Db	219	acatgatcacatcacctgtactccagcctgggttgacagagtgaagccctgltcctcaaaaaa	278
Cp	1125	CCATGTTGTGTCTCACTGCACCTCCAGCCCTGGGTGTGACAGAGTGAAGCCCTGTCAAAAAAAA	1066

[illegible]

LOCUS	388 bp	EST	U3-APR-1995
KB0116		mRNA	
DEFINITION	ye89b09.r1 Homo sapiens cDNA clone 124889 5' similar to contains		
Alu repetitive element?.			

ACCESSION	R06116
NID	9756736
KEYWORDS	FST

ORGANISM	SOURCE
Homo sapiens	human clone-124889 library-Soares fetal liver spleen INFES vector-p17T33 (Pharmacia) with a modified polylinker host-CDH10B (ampicillin resistant) primer-M13P1 RstI-e1-Pac I RstI-e2-Eco RI liver and spleen from a 20 week-post conception male fetus. 1st strand cDNA was primed with a Pac I - Oligo(dT) primer [5' AACCTGGAGAGATTAATTAAGAATCTTTTATTTTTTTTTT 3'], double-stranded cDNA was ligated to Eco RI adaptors (Pharmacia), digested with Pac I and cloned into the Pac I and Eco RI sites of the modified pT73 vector. Library went through one round of normalization. Library constructed by Bento Soares and M.Fatima Bonaldo.

Eucairioetes; Metazoa: Chordata; Vertebrata; Gnathostomata; Mammalia
Eutheria; Primates; Carnivora; Homiidae; Homo.
1 (bases 1 to 388)
Hillis, D.M., Clark, A.G., Duboucq, T., Elliston, K., Hawkins, M.,

TITLE
JOURNAL
COMMENT

The Washu-Mercer EST Project
Unpublished (1995)

Contact: Wilson RK
Washu-Merck EST Project
Washington University School of Medicine
444 Forest Park Parkway, Box 8501, St. Louis, MO 63108
Tel.: 314 286 1800

FEATURES
 SOURCE
 1..386
 Location/Qualifiers
 Image: 1..386
 Email: estewatson.wustl.edu
 Fax: 314 286 1810
 High quality sequence stops: 312
 Source: IMAGE Consortium, LINTL
 This clone is available royalty-free through LINTL; contact the
 IMAGE Consortium (info@image.lnl.gov) for further information
 Location/Qualifiers
 1..386

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/organism="Homo sapiens"
; /clone="124889"

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BASE COUNT ORIGIN	88 a	92 c	85 g	120 t	3 others
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Best Local Similarity	75.8%;	Pred. No. 1.15e-100;		
Matches 188;	Conservative 0;	Mismatches 58;	Indels 2;	Gaps 2

Db 134 ttttttttttttgcagacaggtctcactctgtcacccagctnagtacagtatgtg 193
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[illegible]

REFERENCE	Eukaryote; mitochondrial eukaryotes: Metazoa: Chordata: Vertebrata: Eutheria: Primates; Catarrhini: Hominoidea: Homo.
AUTHORS	1 (bases 1 to 571) Hallier,L., Clark,N., Dubuque,T., Elliston,K., Hawkins,M., Holman,M., Hultman,M., Kucaba,T., Le,M., Lennon,G., Marra,M., Parsons,J., Rifkin,L., Rohlfing,T., Tan,F., Trevisakis,E., Waterston,R., Williamson,A., Wohlmann,P. and Wilson,R. WashU-Merck EST Project Unpublished (1995)
TITLE	
JOURNAL	
COMMENT	Contact: Wilson RK WashU-Merck EST Project Washington University School of Medicine 4444 Forest Park Parkway, Box 8501, St. Louis, MO 63108 Tel: 314 286 1800 Fax: 314 286 1810 Email: est@watson.wustl.edu This clone is available royalty-free through LNL ; contact the IMAGE Consortium (info@image.lln.gov) for further information. Seq primer: -40M13 fwd. from Amersham High quality sequence stop: 194. Location/Qualifiers 1..571
FEATURES	
SOURCE	/organism="Homo sapiens" /note="Organ: colon; Vector: pBluescript SK-; Site.1: EcoRI; Site.2: XhoI; Cloned unidirectionally. Primer: Oligo dt. T-84 colonic epithelial cell line. Average insert size: 1.0 kb; Uni-ZAP XR Vector: ~5' adaptor sequence: 5' GAATTCGGCAGCG 3' ~3' adaptor sequence: 5' CTCGAGTTTTTTTTTTTTTTTTTTT 3" /clone="-587046" /clone_id="Stratagene colon (#937204)" /lab_host="SOER cells (kanamycin resistant)" complement(<1..>571)
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ORIGIN	
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Matches	191; Conservative 0; Mismatches 40; Indels 6; Gaps 5;
Db	11 ttttctttatttgagacagggtcttactctgtgtaaccaggcgtgaatgcattggcaag 70
Oy	1059 TTTTCTTTTCTTTTGTGACAGGCTGCATCTGTCACCCAGCTGAGTAGTGAGCGCAC 118
Db	71 atcatggtctaactgtaggtgcacctcccaa-gctccaagtatatctcccactcaagctc 129
Oy	1119 ACCAAGGCTCTCTGAGCGCTTGACTCTGGAGGCAAGTAATCCTCGCTCATGTC 1178
Db	130 ccacatagctggagcacacaagaatgtagcacacacacgtggctaa-ttttgttat-- 186
Oy	1179 CT-ACTACTGGAACATAAGAAGAGGCCACCACACCTGACTAACTTTTGTGTTTTGT 1237
Db	187 ttg-tagagacaaggttttgccatgttggccaagcgtagtcttgaaactcccaagctca 242
Oy	1238 TTGGTAAAGATGGCATTTGCCCATGTGTGTACAGGCTGTGTCAAACTCTCTAGGTCA 1294
RESULT	9
LOCUS	R44830 353 bp mRNA EST 22-MAY-1995
DEFINITION	y931d01.s1 Homo sapiens cDNA clone 34159 3' similar to contains Alu repetitive element;.
ACCESSION	R44830
NID	9824206
KEYWORDS	EST.
SOURCE	human clone-34159 library-Sources infant brain INTB vector-Lafmid BA host-DH10B (ampicillin resistant) primer-Promega -2ml3 Rsife2-Not I Rsife2-Hind III Whole brain from a 73 days post natal female. 1st strand cDNA was primed with a Not I - Oligo(dt) primer (5' AACTGCAGAGATTTCGGCGCCGACGGAATTTTTTTTTTTTTTTT 3'); double-stranded cDNA was ligated to Hind III adaptors (Pharmacia), digested with Not I and directionally cloned into the Not I and Hind III sites of the Lafmid BA vector. Library went through one round of

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KEYWORDS EST.
SOURCE human.
ORGANISM Homo sapiens
REFERENCE Eukaryotae; mitochondrial eukaryotes; Metazoa; Chordata; Vertebrata; Eutheria; Primates; Catarrhini; Hominiini; Homidae; Homo. 1 (bases 1 to 300)
AUTHORS Hillier, L., Clark, N., Dubuque, T., Elliston, K., Hawkins, M., Holman, M., Hultman, M., Kucaba, T., Le, M., Lennon, G., Marra, M., Parsons, J., Rifkin, L., Rohlfing, T., Soares, M., Tan, F., Trevisanski, E., Waterston, R., Williamson, A., Woldmann, P. and Wilson, R.
TITLE The Mashu-Merck EST Project
JOURNAL Unpublished (1995)
COMMENT
Contact: Wilson RK
Mashu-Merck EST Project
Washington University School of Medicine
4444 Forest Park Parkway, Box 8501, St. Louis, MO 63108
Tel: 314 286 1800
Fax: 314 286 1810
Email: est@watson.wustl.edu
This clone is available royalty-free through LINT; contact the IMAGE Consortium (info@image.llnl.gov) for further information.
Putative full length read
The vector to vector length is
Seq primer: -28mb rev2 ET from Amersham.
Location/Qualifiers
1..300

BASE COUNT	86 a	71 c	77 g	66 t
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146	100%			
147	100			

REFERENCE	TITLE	JOURNAL	COMMENT
<p>1 (bases 1 to 447)</p> <p>Hillier, L., Clark, N., Dubaque, T., Elliston, K., Hawkins, M., Holman, M., Hultman, M., Kucaba, T., Le, M., Lennon, G., Matra, M., Parsons, J., Rifkin, L., Rohlfing, T., Tan, F., Trevasaks, B., Waterston, R., Williamson, A., Wohlmann, P. and Wilson, R.</p> <p>Washu-Merck EST Project</p> <p>Unpublished (1995)</p>	<p>element MER22 repetitive element ;</p> <p>Human.</p> <p>Human sapiens</p> <p>Eukaryotae; mitochondrial eukaryotes; Metazoa; Chordata; Vertebrata; Mammalia; Eutheria; Primates; Catarrhini; Homidae; Homo.</p>	<p>AA127449</p> <p>91686789</p> <p>EST.</p> <p>SOURCE</p> <p>ORGANISM</p>	<p> <p>Contact: Wilson RK</p> <p>Washu-Merck EST Project</p> <p>Washington University School of Medicine</p> <p>4444 Forest Park Parkway, Box 8501, St. Louis, MO 63108</p> <p>Tel: 314 286 1800</p> <p>Fax: 314 286 1810</p> <p>Email: est@watson.wustl.edu</p> <p>This clone is available royalty-free through LNL ; contact the IMAG Consortium (info@image.llnl.gov) for further information.</p> <p>Insert Length: 511 Std Error: 0.00</p> <p>Seq Primer: -40M13 fwd. from Amersham</p> <p>High quality sequence stop: 409.</p> </p>

[illegible]

KEYWORDS
EST(expressed sequence tag).

SOURCE
Homo sapiens human pancreatic islets cDNA to mRNA, clone_11b:Human pancreatic islet cDNA clone:hbc5534.

ORGANISM
Homo sapiens
Eukaryote; mitochondrial eukaryotes; Metazoa; Chordata;
Vertebrata; Mammalia; Eutheria; Primates; Carnivora; Homnidae;

REFERENCE
AUTHORS Takeda,J.
TITLE not determined
JOURNAL Unpublished (1996)
REFERENCE 2 (bases 1 to 514)
AUTHORS Takeda,J.
TITLE Direct Submission

COMMENT
Submitted (08-MAY-1996) to the DDBJ/EMBL/GenBank databases. Jun Takeda, Institute for Molecular and Cellular Regulation, Giumma University, Dept. of Molecular Medicine, 3-39-15 Shova-machi, Meibashi 371, Japan (E-mail:j.takeda@meiji.ac.jp,
Tel:+81-272-20-8856, Fax:+81-272-20-8896)
Project='Human pancreatic islet cDNA'
vector-Lambda ZAPIT
primer-T7 primer
Rsited=Eco RI
Rsited=Xho I
mRNA was prepared from normal adult human islets. cDNA was directionally synthesized from the Xho I in the vector to the EcoRI site.
cDNA was size fractionated to remove sequences <1000 bp in size.

FEATURES
source
1..514
/organism="Homo sapiens"
/clone="hbc5534"
/clone_11b="Human pancreatic islet cDNA"
/tissue_type="human pancreatic islets"

BASE COUNT
113 a 158 c 96 g 143 t 4 others

ORIGIN

Query Match 7.5%; Score 106; DB 91; Length 514;
Best Local Similarity 76.1%; Pred. No. 8.32e-105;
Matches 175; Conservative 0; Mismatches 52; Indels 3; Gaps 3;

Db	1	ttttttatttttgagacgagctgtgcctgtgtcccaaggctgagtcagtcagcagc	60
OY	1059	TTTTTTT TTTT TTTTGACAGGGGTCTACTGTCATACCAGGCTGGAGTGCAGTGGCAC	1118
Db	61	atcttgtctactgcgaagctccaccctccag-gtccaagccattctctgcctccagctc	119
OY	1119	ACCAAGGCTCTCTGACGCTTGACCTCGGGAGCTCAGAAGTGAATCCCTCGCCTCAGTCTC	1178
Db	120	ccaagttagctgagctacagatgcccccacaccccccggttaattttttttgtatt-t	178
OY	1179	CTA-GTACTCTGAACTACAAGAGAGGGCCACACACCTGACCTTAATTTTGTGTTTGT	1237
Db	179	ttagtanagatggggtttcaccatgtttagcagaagttgtctcagctctt	228
OY	1238	TTCGTAAGATGGCATTTGCCCATGTTCTACAGGCTGCTCAAACTCCT	1287

RESULT
LOCUS AA226159 465 bp mRNA EST 01-MAY-1997
DEFINITION ncl0h07.1 NCI CGAP P11 Homo sapiens cDNA clone 1910 similar to contains Alu repetitive element.
ACCESSION AA226159
NID q1847475
KEYWORDS EST.
SOURCE human.
ORGANISM Homo sapiens
Eukaryote; mitochondrial eukaryotes; Metazoa; Chordata;
Vertebrata; Mammalia; Eutheria; Primates; Carnivora; Homnidae;
Homo.
REFERENCE 1 (bases 1 to 465)
NCI-CGAP.
National Cancer Institute, Cancer Genome Anatomy Project (CGAP),

JOURNAL
Tumor Gene Index
Unpublished (1997)

COMMENT

Contact: Robert Strausberg, Ph.D.
Tel: (301) 496-1550
Email: Robert.Strausberg@nih.gov
Tissue Procurement: W. Marston Linehan, M.D., Rodrigo Chuagui,
M.D., Michael Emmert-Buck, M.D., Ph.D.
CDNA Library Preparation: David B. Kitzman, Ph.D.
CDNA Library Arrayed by: Genome Systems Inc., Greg Lennon, Ph.D.
DNA Sequencing by: Washington University Genome Sequencing Center
clone distribution: NCI-CGAP clone distribution information can be
found through the I.M.A.G.E. Consortium/ILM at:
www-bio.lnl.gov/db/rrp/image/image.html
For additional information: Robert Strausberg, Ph.D.
Phone: (301) 496-1550
E-mail: Robert.Strausberg@nih.gov
Seq primer: -28m13 rev1 Et from Amersham
High quality sequence stop: 330.

FEATURES

source

1..465
/organism="Homo sapiens"
/note="Vector: PAMF10; Site.1: Not1; Site.2: EcoRI; 1st
strand cDNA was primed with oligo(dT)17 on 50 ng of
DNase-treated, total cellular RNA obtained from
5,000-10,000 microdissected, histologically normal
prostate epithelial cells. Double-stranded cDNA was
ligated to EcoRI adaptors, 5 cycles of PCR applied to the
cDNA with an adaptor-specific primer, and the resulting
PCR product subcloned into PAMF10 by the UPG-cloning
method (Life Technologies). Average insert size is 600
bp. NOTE: Not directionally cloned. This library was
constructed by David Kitzman."
/clone="1910"
/clone.lib="NCI CGAP Pri1"
/sex="Male"
/dev.stage="45 years old"
/lab_host="DH10B"
<1..>465

BASE COUNT

130 a 86 c 133 g 116 t

ORIGIN

Query Match 7.4%; Score 105; DB 71; Length 465;
Best Local Similarity 74.08; Pred. No. 2,13e-103;
Matches 185; Conservative 0; Mismatches 62; Indels 3; Gaps 3;

Db 217 ggggggagtcattggagcccatgagttcagacagctagctggggaacatagtgaagccctgt 276
|||||
Cp 1306 gggagggccaaagtgaaagccttagagcttttgagacacagctcttgcacatgccaataatgccat 1247
Db 277 ctctacacaaatacaaaataaanaaattagctaggtgtgtgtgcacatgacccgtagctcg 336
|||||
Cp 1246 ctttaccacaaacaa-aaaacaaaaaatttagtcagtgtagcgtggtggcccttctttagattcc 1188
Db 337 agctgcttggagagctcgagggcggagagattgcttaag-tccagaagttcagagctcgaag 395
|||||
Cp 1187 agctacacatgag-aaactggaagcaggaagacacactttagagctccacagaggtcacaagctgcaga 1129
Db 396 aaagtagatcatcagcagcagcactccaacttgggtggaagagagcagagccctggttcacaa 455
|||||
Cp 1128 gagcgaatggtgtggtccactgcactccagccttggtgacagatgacagacccctgtcaaaaaa 1069
Db 456 aaaaaaaaaa 465
|||||
Cp 1068 aaaaaaaaaa 1059

RESULT 7

LOCUS AA229986 361 bp mRNA EST 01-MAY-1997

DEFINITION nc37605.s1 NCI CGAP Pri2 Homo sapiens cDNA clone 4450 similar to

ACCESSION AF229986

FEATURES

1..465

ORIGIN

1853280

Db	224	tttagcagagcttggagcttcacccctggttcggcagagctctgtcccaacccct	275
07	1237	TTTG-GTAAAGATGGCATTTCGCATGTGTGTAAGGCGCTGGCTCTCAACTCT	1287
LOCUS	9		
DEFINITION	W93002	384 bp	EST
ACCESSION	Z800D12.s1	Soares fetal liver spleen	INRIS S1 Homo sapiens cDNA
NID	W93002	clone 418391 3'	similar to contains Alu repetitive element;.
KEYWORDS	g1422153		
SOURCE	EST		
ORGANISM	human.		
REFERENCE	Homo sapiens		
THORNS	Eukaryotae: mitochondria		eukaryotes; Metazoa; Chordata; Vertebrata; Mammalia; Eutheria; Primates; Catarrhini; Homiidae; Homo.
	1 (bases 1 to 384)		
	Hillier, L., Clark, N., Dubuque, T., Elliston, K., Hawkins, M., Holman, M., Hultman, M., Kucaba, T., Le, M., Lennon, G., Marra, M., Parsons, J., Rifkin, L., Rohlfing, T., Tan, F., Trevisakis, E., Waterston, R., Williamson, A., Wohlmann, P., and Wilson, R.		
TITLE	WashU-Merck EST Project		
JOURNAL	Unpublished (1995)		
COMMENT			

Contact: Wilson RK
 Washu-Merck EST Project
 Washington University School of Medicine
 4444 Forest Park Parkway, Box 8501, St. Louis, MO 63108
 Tel: 314 286 1800
 Fax: 314 286 1810
 Email: est@watson.wustl.edu
 This clone is available royalty-free through LIND¹; contact the
 IMAGE Consortium (image@iml.gov) for further information.
 Insert length: 751 Std Error: 0.00
 Seq primer: mob.REGA+ET
 High quality sequence stop: 340.
 Location/Qualifiers
 1..384

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/organism="Homo sapiens"
/note="Organ: Liver and Spleen; Vector: p773D (Pharmacia)
with a modified polylinker; Site.1: Pac I; Site.2: Eco RI
This is a subtracted version of the original Soares fetal
liver spleen INFLS library. 1st strand cDNA was primed
with a Pac I - oligo(dT) primer [5',
AATCGAGAGAAATATATAGATCTTTTGTGTGTGTGTGT 3'],
double-stranded cDNA was ligated to Eco RI adaptors
(Pharmacia), digested with Pac I and cloned into the Pac
and Eco RI sites of the modified p773 vector. Library
went through one round of normalization. Library
constructed by Bento Soares and M.Fatima Bonaldi."
/clone="418391"
/clone_lib="Soares fetal liver spleen INFLS S1"
/sex="male"
/dev_stage="20 week-post conception fetus"
/lab_host="DH10B (ampicillin resistant)"
complement<1..>384"
/db_xref="GDB:1326861"

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Best Local Similarity	72.5%;	Pred. No. 5,43e-102;		
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Db	3	gaagagatctactcctgtgcccagaatgatggatcaattgtttgcatacacagcatctgc	62	
OY	1075	GACAGGGCTTCACTGTGCACCACGCGTGAGATGAGTCACAC -CATGGCTCTTGC	1133	
Db	63	aggctacacctcttgga-ctcaagaacatctcttcacatccagctccocctagttagctagc	121	
OY	1134	AGCCTTAGCCCTTGAGGAAGCTCAAGTAGATCTCTCTGCTCAAGTTTC -TAGTAGCTGGAAC	1192	

Db 122 caccggttcgcccacacgatacctcgtatacatlitttggtlitttttg-tagaatggg 180
Qy 1193 TACAAGGAAGAGGCGCACCAACCCGAGACTACTTTTGTGTGTGTGTAAGATGGCA 1252
Db 181 tcttcctatgttcccatgtgtgtcttgaacccctgggctcaagatgacccccaagt 240
Qy 1253 TTTTGCCATGTGTGACAGGCGTGGTTCGAACACTCGATGCTTCTGGCCTCCCAAGTG 1312
Db 241 ctgggattacagagcttcagcaantctgctctggc 273
Qy 1313 CTGGGATTACAGACATGACTGCGAAGCCCCGGC 1345

RESULT	10	AA386111	426 bp	mRNA	EST	21-APR-1997
LOCUS		ES070725	Brain IV	Homo sapiens	CDNA similar to EST containing Alu	
DEFINITION		repeat.				
ACCESSION		AA386111				
NTID		G2038587				
KEYWORDS		EST.				
SOURCE		human.				
ORGANISM		Homo sapiens				

REFERENCE	AUTHORS
1 (bases 1 to 426)	
Adams,M.D., Kerlavage,A.R., Fleischmann,R.D., Fulder,R.A.,	Bult,C.J., Lee,N.H., Kirkness,E.F., Weinstock,K.G., Gocayne,J.D.,
White,O., Sutton,G., Blake,J.A., Brandon,R.C., Maniwal,C.,	Clayton,R.A., Cline,T.R., Cotton,M.D., Earle-Hughes,J., Fine,L.D.,
Fitzgenzard,L.W., Fitzhugh,W.M., Fritchman,U.L., Geoghagen,N.S.,	Glodok,A., Gnehm,C.L., Hanna,M.C., Hedblom,E., Hinkle,P.S., Jr.,
Kelley,J.M., Kelley,J.C., Liu,L.-I., Matmaros,S.M., Merrick,J.M.,	Moreno-Palmarques,R.F., McDonald,L.A., Nguyen,D.T., Pelligrino,S.M.,
Phillips,C.A., Ryder,S.E., Scottb,T.L., Saudak,D.M., Shirley,R.,	Small,K.V., Spriggs,T.A., Utterback,T.R., Weidman,J.F., Wiley,
Bednarzik,D.P., Cao,L., Cepeda,M.A., Coleman,T.A., Collins,E.J.,	Dimke,D., Fung,D.-F., Ferrite,A., Fischer,C., Hastings,G.A.,
He,W.W., Hu,J.-S., Greene,U.M., Gruber,J., Hudson,P., Kim,A.K.,	Kozak,D.L., Kunsch,C., Hungjun,J., Li,H., Meisner,P.S., Olsen,H.,
Raymond,L., Wei,Y.F., Wang,J., Xu,C., Yu,G.L., Ruben,S.M.,	Dillion,P.J., Fannon,M.R., Rosen,C.A., Haseltine,W.A., Fields,C.,
Fraser,C.M. and Venter,J.C.	
TITLE	
Initial assessment of human gene diversity and expression patterns	
based upon 83 million nucleotides of cdna sequence	
Journal Nature 377 (6547 Suppl), 3-174 (1995)	
96026280	
Other_ENTS: EST01568 TRC110460	

Contact: Kerlavage, AR
Bioinformatics
The Institute for Genomic Research
9712 Medical Center Drive, Rockville, MD 20850 USA
Tel.: 3018699056
Fax: 3018698423
Email: arkerlav@tigr.org
For clone availability, additional sequence and expression
information related to this EST, please check the TIGR Human Gene
Index (<http://www.tigr.org/cdb/hgi/hgi.html>)
Seq primer: M13-21.

FEATURES	SOURCE	Location/Qualifiers
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		/dev_stage="fetus, 17-18 wks"
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Query Match	7.3%	Score 104; DB 62; Length 426;

[illegible][illegible]

	RESULT	14	C15363	351 bp	mRNA	EST	03-SEP-1996
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	DEFINITION		Human fetal brain cDNA 5'-end	GEN=J137E09.			
	ACCESSION		C15363				
	NID		g1570070				
	KEYWORDS		Est(expressed sequence tag); Human fetal brain.				
	SOURCE		Homo sapiens fetus brain cDNA to mRNA, clone:J137E09.				
	ORGANISM		Homo sapiens				
			Eukaryote; mitochondrial eukaryotes; Metazoa; Chordata;				
			Vertebrata; Mammalia; Eutheria; Primates; Catarrhini; Homiidae;				
	REFERENCE		Homo				
	AUTHORS		1 (sites)				
			Fujiwara,T., Hirano,H., Hishigaki,H., Horie,M., Kawai,A., Kuga,Y., Kyushiki,I., Nagata,M., Okuno,S., Ozaki,K., Shimizu,F., Shimada,Y., Shinomiya,H., Suzuki,M., Takachi,A., Takeda,S., Watanabe,T., Maekawa,H., Nakamura,Y. and Takahashi,E.				
	TITLE		Otsuka cDNA project				
	JOURNAL		Unpublished (1996)				
	REFERENCE		2 (bases 1 to 351)				
	AUTHORS		Fujiwara,T.				
	TITLE		Direct Submission				
	JOURNAL		Submitted (13-MAY-1996) to the DDBJ/EMBL/Genbank databases. Teutomu Fujiwara, Otsuka GEN Research Institute,Otsuka Pharmaceutical Co.,Ltd: 463-10 Kagasuno Kawamuchi-cho, Tokushima, Tokushima 771-01,				
			Japan (Tel:+81-886-65-2888, Fax:+81-886-37-1035)				
	FEATURES		Location/Qualifiers				
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BASE COUNT			90 a	86 c	67 g	98 t	10 others
ORIGIN							
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Best Local Similarity			76.2%;	Pred.No.2,2le-96;			
Matches 176;	Conservative		7;	Mismatches 41;	Indels 7;	Gaps 4;	
Db	116 bdbbttyttttttttaagacagatctcactctgttcacccaggctgaagtgcagtggcgc	175	::::: :	:	: :	:	
cy	1058 ctttttttttttttttgacagggtctcacctctgtccaccacgggtcgattcaatggcgc	1117	:	:	:	:	

[illegible]

LOCUS	15	RESULT
DEFINITION	AA195351	379 bp mRNA EST 14-FEB-1997
DESCRIPTION	zr33p12.s1	Soares NHMPU SI Homo sapiens cDNA clone 665254 3
COMMENTARY		similar to contains Alu repetitive element.

EST. human.
Homo sapiens

REFERENCE
AUTHORS
Hillier, L., Clark, N., Dubuque, T., Elliston, K., Hawkins, M.,
1 (bases 1 to 379)
Eukaryotae; Eukaryotae; Metazoa; Chordata;
Vertebrata; Eutheria; Primates; Catarrhini; Hominoidea; Homo
1 (bases 1 to 379)

TITLE	COMMENT
The Washu-Merck EST Project Unpublished (1995)	

Contact: Wilson RK
WashU-Merck EST Project
Washington University School of Medicine
4444 Forest Park Parkway, Box 8501, St. Louis, MO 63108
Tel: 314 286 1800
Fax: 314 286 1810
Email: estewartson.wustl.edu
This clone is available royalty-free through LNL; contact the
IMAE Consortium (info@image.lnl.gov) for further information
High quality sequence stop: 271.

FEATURES
source

1..379

/organism="Homo sapiens" /note="Organ: mixed (see below): Vector: pT73D-Pac (Pharmacia) with a modified polylinker; Site_1: Not I; Site_2: Eco RI; Equal amounts of plasmid DNA from three normalized libraries (melanocyte 2NH9, pregnant uterus NbH9U, and fetal heart NbH9H15) were mixed, and ss circles were made in vitro. Following NspI purification, this DNA was used as tracer in a subtractive hybridization reaction. The driver was PCR-amplified cDNAs from pools of 5,000 clones made from the same 3 libraries. The pools consisted of L.M.A.G.E. clones 260323-265223, 340488-345479, and 484488-489479."

BASE COUNT	ORIGIN	complement(<1..>379)	114 t
75 a	103 c	87 g	.

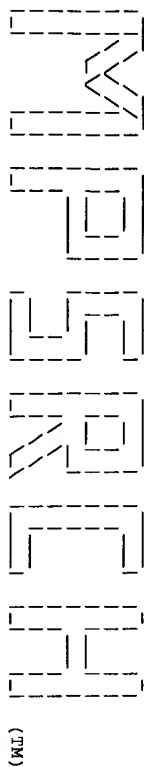
Query Match	7.1%;	Score 100;	DB 2;	Length 379;
Best Local Similarity	78.5%;	Pred. No. 2.21e-96;		
Matches	186;	Conservative	0;	Mismatches 44;
			Indels	7;
			Gaps	4;

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        |||||
QY    1059 tttttttttttttttgacagaggttcacctgtcaccaccaggctggaaatgcagtgccacc 1118
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[illegible]

Search completed: Wed Mar 25 13:54:24 1998
Job time : 470 secs.

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Release 2.1D John F. Collins, Biocomputing Research Unit.
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Distribution rights by Intelligentics, Inc.

Mpsrch_nun n.a. - n.a. database search, using Smith-Waterman algorithm
Run on: Wed Mar 25 12:55:36 1998; Maspar time 1516.90 Seconds
1325.012 Million cell updates/sec
Blar output not generated.

Title: >US-08-236-918A-7
Description: (1-1415) from 5674704.seq
Perfect Score: 1415
N.A. Sequence: 1 AGTGAAGATCTCCGCGAC.....TGANAAAAAAAAAAAAA 1415
Comp: TCACCTTCAAGAGCCGTC.....ACATATTTTATTTTATTTT

Scoring table:

TABLE default
Gap 6

Nmatch STD : Dbase 0; Query 0

Searched: 430261 seqs, 710217276 bases x 2

Post-processing: Minimum Match 08
Listing first 45 summaries

Database:

embl-new7
1.BCT 2.FUN 3.GEN 4.HTG1 5.HTG2 6.HTG3 7.HTG4 8.HUM1
9.HUM2 10.HUM3 11.INV1 12.INV2 13.ORG 14.MAM 15.VRT
16.PLN 17.PRO1 18.PRO2 19.ROD 20.SYN 21.UNC 22.VIR
genbank101
23.BCT1 24.BCT2 25.BCT3 26.BCT4 27.BCT5 28.BCT6 29.BCT7
30.BCT8 31.BCT9 32.BCT10 33.BCT11 34.BCT12 35.BCT13
36.GEN1 37.GEN2 38.GEN3 39.GEN4 40.GEN5 41.GEN6 42.HTG1
43.HTG2 44.HTG3 45.HTG4 46.HTG5 47.INV1 48.INV2 49.INV3
50.INV4 51.INV5 52.INV6 53.INV7 54.INV8 55.INV9 56.INV10
57.INV11 58.INV12 59.MAM1 60.MAM2 61.MAM3 62.VRT1
63.VRT2 64.VRT3 65.VRT4 66.PAT1 67.PAT2 68.PAT3 69.PAT4
70.PAT5 71.PAT6 72.PAT7 73.PHG 74.PHG1 75.PHG2 76.PHG3
77.PHG4 78.PHG5 79.PHG6 80.PHG7 81.PHG8 82.PHG9 83.PHG10
84.PHG11 85.PHG12 86.PHG13 87.PHG14 88.PHG15 89.PHG16
90.PHG17 91.PHG18 92.PHG19 93.PHG20 94.PHG21 95.PHG22
96.PHG23 97.PHG24 98.PHG25 99.PHG26 100.PHG27 101.PHG28
102.PHG29 103.PHG30 104.PHG31 105.PHG32 106.PHG33 107.PHG34
108.PHG35 109.PHG36 110.PHG37 111.PHG38 112.PHG39 113.PHG40

Database:

genbank101
115.VRL1 116.VRL2 117.VRL3 118.VRL4 119.VRL5 120.VRL6
121.VRL7 122.VRL8 123.VRL9 124.VRL10 125.VRL11
genbank-new7
126.BCT 127.GEN 128.HTG1 129.HTG2 130.INV 131.MAM
132.VRT 133.PHG 134.PLN 135.PLN2 136.PRI1 137.PRI2
138.ROD 139.SYN 140.UNA 141.VRL
u-embl51_101
142.part1 143.part2

Database:

Database:

Database:

Statistics: Mean 11.786; Variance 6.409; scale 1.839

Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,

and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB	ID	Description	Pred. No.
1	1415	100.0	1415	94	HSU03397	Human receptor protel	0.00e+00
2	1378	97.4	1419	99	HUM1LAX	Human activation depe	0.00e+00
3	233	16.5	2350	108	MSTCQ41BR	Mouse T-cell receptor	1.00e-145
4	131	9.3	940	101	HUMTRPM2A2	Human TRPM-2 protein	5.04e-69
5	129	9.1	1583	95	HS390013	Human DNA sequence **	5.94e-68
6	126	8.9	100234	128	HS341D10	Human DNA sequence **	9.12e-66
7	126	8.9	100234	5	HS341D10	Human DNA sequence **	9.12e-66
8	124	8.8	8339	8	HSAB1901	Human DNA sequence **	9.12e-66
9	124	8.8	32351	99	HSM167P19	Human gene for L-hist	4.87e-65
10	125	8.8	100000	45	HSAC12	*** SEQUENCING IN PRO	4.87e-65
11	125	8.8	100000	5	HSAC12	*** SEQUENCING IN PRO	4.87e-65
12	125	8.8	100000	5	HSAC12	*** SEQUENCING IN PRO	4.87e-65
13	124	8.8	145194	5	HS339A18	Human DNA sequence **	2.60e-64
14	124	8.8	145194	128	HS339A18	Human DNA sequence **	2.60e-64
15	121	8.6	96625	89	HSAC000118	Human BAC clone RG072	3.90e-62
16	121	8.6	112601	45	HS60N8	Human DNA sequence **	3.90e-62
17	121	8.6	137246	88	HS49J10	Human DNA sequence **	3.90e-62
18	122	8.6	166271	45	HS445C9	Human DNA sequence **	7.35e-63
19	122	8.6	224681	128	HS44N10	Human DNA sequence **	7.35e-63
20	122	8.6	224681	5	HS44N10	Human DNA sequence **	7.35e-63
21	122	8.6	225094	42	AC002044	*** SEQUENCING IN PRO	7.35e-63
22	122	8.6	225094	42	AC002044	*** SEQUENCING IN PRO	7.35e-63
23	120	8.5	225094	5	HSAC2044	*** SEQUENCING IN PRO	7.35e-63
24	120	8.5	4699	86	AC002212	Human DNA sequence **	2.07e-61
25	120	8.5	4699	6	HSAC2212	Human DNA sequence **	2.07e-61
26	120	8.5	27584	137	HSB5E3A	Human DNA sequence **	2.07e-61
27	120	8.5	27584	8	HSB5E3A	Human DNA sequence **	2.07e-61
28	120	8.5	100000	0	HSAC11	*** SEQUENCING IN PRO	2.07e-61
29	120	8.5	100000	45	HSAC000011	*** SEQUENCING IN PRO	2.07e-61
30	119	8.4	37027	88	HS006G2B	Human DNA sequence **	1.10e-60
31	119	8.4	43952	94	HSU105G4	Human DNA sequence **	1.10e-60
32	119	8.4	76094	87	HS179D3A	Human DNA sequence **	1.10e-60
33	119	8.4	95425	91	HSJ506G21	Human DNA sequence **	1.10e-60
34	119	8.4	127079	87	HS214K23	Human DNA sequence **	1.10e-60
35	119	8.4	130679	44	HS211D12	Human DNA sequence **	1.10e-60
36	118	8.3	2802	89	HSAC000966	Human DNA sequence **	5.80e-60
37	118	8.3	2854	100	HUMNFI1793	Human NFG genomic fra	5.80e-60
38	118	8.3	2897	92	HS181575	Human sapiens (sublon	5.80e-60
39	118	8.3	3726	92	HS181575	Human sapiens (sublon	5.80e-60
40	118	8.3	13204	98	HDMGP11B2	Human platelet glycop	5.80e-60
41	118	8.3	13204	98	HS46H23	Human DNA sequence **	5.80e-60
42	118	8.3	132645	129	AC002345	*** SEQUENCING IN PRO	5.80e-60
43	118	8.3	132645	6	HSAC2345	*** SEQUENCING IN PRO	5.80e-60
44	118	8.3	142395	89	HSAC000120	Human BAC clone RG161	5.80e-60
45	118	8.3	210672	44	HS179115	Human DNA sequence **	5.80e-60

ALIGNMENTS

RESULT	LOCUS	DEFINITION	ACCESSION	NID	KEYWORDS	ORGANISM	REFERENCE	AUTHORS	TITLE
1	HSU03397	Human Receptor Protein 4-1BB mRNA, complete cds.	U03397	9571320	human.	human.	Algeron, M.R., Smith, C.A., Tough, T.W., Davis-Smith, T., Armitage, R.J., Falk, B., Roux, E., Baker, E., Sutherland, G.R., Dru, W.S. and Goodwin, R.G.	Journal	Molecular and biological characterization of human 4-1BB and its ligand
									Eur. J. Immunol. 24 (9), 2219-2227 (1994)

TITLE A receptor induced by lymphocyte activation (ILA): a new member of the human nerve-growth-factor/tumor-necrosis-factor receptor family
JOURNAL Gene 134 (2), 295-298 (1993)
MEDLINE 94085794
REFERENCE 2 (bases 1 to 1419)
AUTHORS Schwarz, and H. and H. TITLE Direct Submission.
JOURNAL Submitted (22-APR-1993) Schwarz H., Sam and Rose Stein Institute for Research on Aging, University of California, San Diego, La Jolla, CA 92093-0663, USA

FEATURES
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Location/Qualifiers
/organism="Homo sapiens"
/cell-type="transformed T lymphocyte"
/cell_line="SLB-1"

5' UTR 1..139
gene 140..907
CDS 140..907
/gene="ILA"
/note="ILA" induced by lymphocyte activation; similar to Human receptor protein encoded by GenBank Accession Number U03397"

/codon_start=1
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/translation="MGNSCIYIVATLLIVLNFERTSLQDFCSNCPAGTFCDNNRNOI
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EODRCQDELTKGCKDCDCEFTNDOKGIRPMTNGLSDKSYLVNTEKRDVYCP
SPADLSPGASVTPPARBERGHSPOIISFLALISFLALFLFLRFSVYVRGKR
KLUIFKQPFMRPVQITQEDGCSCRPEEBSGCEL"

3' UTR 908..1419
polyA_signal 1369..1374
polyA_site 1419
BASE COUNT 373 a 340 c 342 g 364 t
ORIGIN

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Best Local Similarity 99.6%; Pred. No. 0.00e+00;
Matches 1394; Conservative 0; Mismatches 4; Indels 2; Gaps 2;

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D 81 ttgataaatctctcttgaaatcagcttctgtagtatacatcctgtgcagaattcatca 140
O 61 TTGATTAATATCTCTTGGAAATCAGCTTGTGATATCATACCTGTGCCAGATTTCATCA 120
D 141 tgggaaacagctgttacacaatagtagcaactctgtctgtgctcctaactttgaggaga 200
O 121 TGGGAAACAGCTGTACAAATAGTAGCCACTGTGTGCTGCTCAACTTTGAGAGGA 180
D 201 caagtcattcagagatcctctgttagtaactcgcacagctgtgtacattcgtgataaaca 260
O 181 CAAGTCATTGCAAGATCTCTGTAGTAACCTGCCAGCTGTGATTCGTGATTAATACA 240
D 261 ggaatcaaatctgacagctccctctcctccaatagtttccagcgacaggttgacaagaaga 320
O 241 GGAATCAATTTGCGATCCCTCTCTCCAAATAGTTTCTCCAGCCAGAGTGAGCAAGA 300
D 321 cctgtgacatactgcagcagagtgtaagggtttttcagagaccagaaagagtgctctca 380
O 301 CCTGTGACATATGACAGGAGAGTAAAGGTGTTTCAGAGCCAGAGAGTGTCTCTCA 360
D 381 ccagcaatgcagagtgtaactgcacccaagggtttcaactgcctggggcagagatgcagca 440
O 361 CCAGCAATGCAGAGTGTACTGCTCACTCCAGGGTTTCACCTGGGGCAGAGATGCACGA 420
D 441 tgtgtgaaacagagtgtagtaagagtgtaagagtaagagtaagagtaagagtgtaagag 500
O 421 TGTGTGAACAGGATGTGTAACAGAGTCAAGATCAACAAAAAGTGTGTAAGACTGTT 480
D 501 gctttggacatttaacagatcagaacgtgcatctgtgcaccctggacaactcttctt 560

O 421 GCTTTGGACATTATACATFCAAGAACTGGCATCTGTGACCTCGGACAACTGTTCTT 540
D 561 tggatgaaagctgtgtgttgtaaggagcaagaagagagagctgtgtgtgacat 620
O 541 TGGATGAAAGCTGTGTGTTGTAATGGAGCAAGAGAGAGAGTGTGTGTGACAT 600
D 621 ctccagccgaactctctccggagagcatctctgtgacccgcgctgcctcgaagaagc 680
O 601 CTCCAGCCGACCTCTCTCCGGAGAGCATCTGTGACCCCGCTGCCCTCGGAGAGAGC 660
D 681 caggacaactcccgagagtaactctctctctctgtgcgtgacgtgcgtgtgctct 740
O 661 CAGGACACTCCCGAGATCAATCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCT 720
D 741 tccgtgttctctctcagcgtccgtctctctgtgtgttaaacggggagaaagaaaccc 800
O 721 TCTGTCTGTTCTTCT 780
D 801 tgtatataatcaaaacacattatagagacagtaacaactactcaagaagagatgact 860
O 781 TGTATATATTCAAACACCATTTATGAGACAGTACAAACTACTCAAGAGAGATGCT 840
D 861 gtactgtccgatttccagaaagaaagagagatgtgaactgtgaaatggaatcaat 920
O 841 GTAGTGGCGGATTTCCAAAGAAAGAGAGAGATGTGAACGTGGAATGGAATCAAT 900
D 921 aggggtgtgtgagacttttgaagaagagcaagaataatagatcatccgtatcaagc 980
O 901 AGGGGTGTGGACTTTCTTGAAGAAAGAGCAAGAAATATGATATCGCTATCACAGC 960
D 981 ttcaaaagcaagaacacacatcctcatataaccagagatcccccacacacagctctt 1040
O 961 TTTCAAAAGCAAGAACACATCTCATATATACCAAGATTCGCCAACACAGCTCTTT 1020
D 1041 tctaaatgccaatgagtggtgaccttaaaatgacacactttttttttttggacag 1100
O 1021 TCTAATGCCAATGAGTGTGGCTTTAAATAATGACACACTTTTTTGTGTTTGTGACAG 1080
D 1101 gtctactctgtaccccgagctgtgagtgtagtgagacacacatgctctctgcagcctg 1160
O 1081 GTCTACTCTGTACCCAGGCTGGAGTGAGTGAGGACACCATGAGCTCTGTGCACCTTG 1140
D 1161 acctgtgagatcaagtgatccctcctcctcagagctctcctagtagctggaactacaag 1220
O 1141 ACCTGTGGAGCTCAAGTATCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCT 1199
D 1221 aagggccacacacactgactaactttttgtttttgtt-ggtaagaatggcattcgc 1279
O 1200 AAGGCCACACACACTGACTAATCTTTTGTGTTTGTGTTGTAAGATGGCATTTGCC 1259
D 1280 atgtgtacagagctgtgtcctcaactcctaggttcaacttggcctcccaagtgtggat 1339
O 1260 ATGTGTACAGAGCTGTGTTCAAACTCTAGGTTCACCTTTGGCCTCCCAAAATGCTG 1319
D 1340 tacagacataagctgacagggccgggccaataatagccacactttaacaaagaagag 1399
O 1320 TACAGACATGAAGTGCAGGCGCCGCGCAAAATATGACACCACTTTTAACAGAACAG 1379
D 1400 atgaggaagagctgtgtat 1419
O 1380 ATGAGGACAGAGCTGTGAT 1399

RESULT 3
LOCUS MUSTC41B 2350 bp mRNA
DEFINITION Mouse T-cell receptor 4-1BB protein mRNA, complete cds.
ACCESSION J04492
NID g201121
KEYWORDS T-cell receptor.
SOURCE Mouse (strain C57BL/6) T-lymphocyte cell lines L2 and L3, cDNA to mRNA.
ORGANISM Mus musculus

RESULT	LOCUS	DEFINITION	ACCESSION	MID	KEYWORDS	SOURCE	ORGANISM	REFERENCE	AUTHORS	TITLE	JOURNAL	COMMENT
5	HS390013	158305 bp	DNA	HTG	22-JAN-1997							
		Human DNA sequence *** SEQUENCING IN PROGRESS *** from clone 390013; HTGS phase 1.										
		284469										
		g1806012										
		HTG: HTGS_PHASE1.										
		human.										
		Homo sapiens										
		Eukaryote; mitochondrial eukaryotes; Metazoa; Chordata; Vertebrata; Eutheria; Primates; Catarrhini; Hominidae; Homo.										
		1 (bases 1 to 158305)										
		Vaudin,M.										
		Direct Submission										
		Submitted (06-NOV-1996) Wellcome Trust Genome Campus, Hinxton, Cambridgeshire, CB10 1SA, UK. E-mail enquiries: humquery@sanger.ac.uk Clone request: clonerequest@sanger.ac.uk IMPORTANT: This sequence is unfinished and does not necessarily represent the correct sequence. Work on the sequence is in progress and the release of this data is based on the understanding that the sequence may change as work continues. The sequence may be contaminated										
		With foreign sequence from E.coli, yeast, vector, phase etc. Order of segments is not known; 800 n's separate segments. Unfinished										
		sequence: d3j90013	Contig_ID: 00607	length: 5173 bp	Unfinished							
		sequence: d3j90013	Contig_ID: 01014	length: 1883 bp	Unfinished							
		sequence: d3j90013	Contig_ID: 00221	length: 1122 bp	Unfinished							
		sequence: d3j90013	Contig_ID: 00328	length: 11779 bp	Unfinished							
		sequence: d3j90013	Contig_ID: 00656	length: 6565 bp	Unfinished							
		sequence: d3j90013	Contig_ID: 00423	length: 2789 bp	Unfinished							
		sequence: d3j90013	Contig_ID: 00388	length: 1089 bp	Unfinished							
		sequence: d3j90013	Contig_ID: 00236	length: 2835 bp	Unfinished							
		sequence: d3j90013	Contig_ID: 00735	length: 3330 bp	Unfinished							
		sequence: d3j90013	Contig_ID: 00491	length: 2332 bp	Unfinished							
		sequence: d3j90013	Contig_ID: 00685	length: 1160 bp	Unfinished							
		sequence: d3j90013	Contig_ID: 00623	length: 1554 bp	Unfinished							
		sequence: d3j90013	Contig_ID: 00030	length: 2127 bp	Unfinished							
		sequence: d3j90013	Contig_ID: 00158	length: 3524 bp	Unfinished							
		sequence: d3j90013	Contig_ID: 00800	length: 1506 bp	Unfinished							
		sequence: d3j90013	Contig_ID: 00618	length: 1016 bp	Unfinished							
		sequence: d3j90013	Contig_ID: 00340	length: 2910 bp	Unfinished							
		sequence: d3j90013	Contig_ID: 00084	length: 6914 bp	Unfinished							
		sequence: d3j90013	Contig_ID: 00948	length: 1080 bp	Unfinished							
		sequence: d3j90013	Contig_ID: 01083	length: 2156 bp	Unfinished							
		sequence: d3j90013	Contig_ID: 00489	length: 3945 bp	Unfinished							
		sequence: d3j90013	Contig_ID: 00583	length: 1508 bp	Unfinished							
		sequence: d3j90013	Contig_ID: 01063	length: 2337 bp	Unfinished							
		sequence: d3j90013	Contig_ID: 00716	length: 6262 bp	Unfinished							
		sequence: d3j90013	Contig_ID: 00671	length: 812 bp	Unfinished							
		sequence: d3j90013	Contig_ID: 00231	length: 859 bp	Unfinished							
		sequence: d3j90013	Contig_ID: 00191	length: 1457 bp	Unfinished							
		sequence: d3j90013	Contig_ID: 00683	length: 918 bp	Unfinished							
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		sequence: d3j90013	Contig_ID: 00435	length: 2095 bp	Unfinished							
		sequence: d3j90013	Contig_ID: 00915	length: 1659 bp	Unfinished							
		sequence: d3j90013	Contig_ID: 00525	length: 2032 bp	Unfinished							

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sequence: dj390013 Contig_ID: 01019 Length: 3698 bp.
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*** WARNING: Phase 1 High Throughput Genome Sequence ***
* This sequence is unfinished. When sequencing is complete,
* the sequence data presented in this record will be replaced
* by a single finished sequence with the same accession number.
Location/Qualifiers
1..158305
 /organism="Homo sapiens"
 /clone="j390013"
 /chromosome="X"

BASE COUNT      35945 a   24148 c   23618 g   36900 t   37694 others

ORIGIN
Query Match          9.1%; Score 129; DB 45; Length 158305;
Best Local Similarity 78.3%; Pred. No. 5,94e-66;
Matches 184; Conservative 0; Mismatches 50; Indels 1; Gaps 1;

Db 133120 ttctctttttttagaacaggccttgctctgtcaactagctgtagtgcagtgtgat 133179
Oy 1061 TTTTCTTTTTTTTGACAGGGGTCCTCACCCTGTCAACCAGGCTGAGTAGTCAGCACAC 1120
Db 133180 catgatttcacgcagccctcgagcctcccaggctaagtgatgcccccacaatacagccccct 133239
Oy 1121 CATGGCTCTCGACGCCCTTGACTCTTGAGGACTCAAGAATGCCTCCGCTCAAGTCTCT 1180

Db 133240 gagtcgcgggaactacaagtgcgtgcacctaacactggtctaatttgtattctctttg 133299
Oy 1181 -AGTAGCGTGAACATCAAGAAAGGCGCACACACTACTACTAACATTCTTTGTTTGTGTTT 1239

Db 133300 ngtagaagatggggtttcaccatatgtggcaggctggtctcaaaactcctggagctaa 133354
Oy 1240 GGTAAGAAGATGGCATTTCCGCATGTTGTACAGAGCTGATGCTCAAACCTCAAGGTTCA 1294

RESULT 6 HS34ID10 100234 bp DNA HTG 22-JUL-1997
LOCUS Human DNA sequence *** SEQUENCING IN PROGRESS *** from clone
DEFINITION 34ID10; HTGS phase 1.
ACCESSION 297985
NID g2274953
KEYWORDS HTG; HTGS_PHASE1.
SOURCE human.
ORGANISM Homo sapiens
Eukaryotes; mitochondrial eukaryotes; Metazoa; Chordata;
Vertebrata; Mammalia; Eutheria; Primates; Catarrhini; Homnidae;
Homo.
1 (bases 1 to 100234)
REFERENCE 1 (bases 1 to 100234)
AUTHORS Buck,D.
TITLE Direct Submission
JOURNAL Submitted (20-JUL-1997) Wellcome Trust Genome Campus, Hinxton,
Cambridgeshire, CB10 1SA, UK. E-mail enquires:
humangery@anger.ac.uk Clone requests: clonerequest@anger.ac.uk
IMPORTANT: This sequence is unfinished and does not necessarily
represent the correct sequence. Work on the sequence is in progress
and
the release of this data is based on the understanding that the
sequence may change as work continues. The sequence may be
contaminated
with foreign sequence from E.coli, yeast, vector, phage etc. Order
of segments is not known; 800 n's separate segments. Unfinished
sequence: dj34ID10 Contig_ID: 00214 Length: 49412 bp Unfinished
sequence: dj34ID10 Contig_ID: 00359 Length: 50022 bp.
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*** WARNING: Phase 1 High Throughput Genome Sequence ***
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* This sequence is unfinished. When sequencing is complete,
* the sequence data presented in this record will be replaced
* by a single finished sequence with the same accession number.
Location/Qualifiers
1..100234
 /organism="Homo sapiens"

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sequence: djl67P19 Contig_ID: 00982 Length: 4726 bp Unfinished
sequence: djl67P19 Contig_ID: 00989 Length: 843 bp.
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*** WARNING: Phase 1 High Throughput Genome Sequence ***
***
* This sequence is unfinished. When sequencing is complete,
* the sequence data presented in this record will be replaced
* by a single finished sequence with the same accession number.
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source
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/organism="Homo sapiens"
/clone="167P19"
/chromosome="X"

BASE COUNT 27173 a 17764 c 18531 g 29152 t 32872 others
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Best Local Similarity 81.7%; Pred. No. 9,12e-66;
Matches 188; Conservative 0; Mismatches 38; Indels 4; Gaps 4;

Db 121496 aggaagtcgagaccagctctgagcaacatggcaaacccgctctac-aaa-aaaaata 121553
CP 1287 AGGAGTTTGAGACCGACGCTGTACACATGGCGAATGCCATCTTACCAACAAACAAACA 1228
Db 121554 gaaataatgacagagtggtggtgcatgtgcctgagtcgccagctaccagagagctgagc 121613
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Db 121614 tggagagatcactatgagc-ccaaagaggtgcagagctgagtgagctgagtggtccagc 121672
CP 1168 CAGAGAGATCATCTTGAGCTCCAGAGAGTCAAGCTGCAGAGAGCCAGTGGTCCACTG 1109
Db 121673 cactccagcttgagtgacagagcagagcctgtctcaaaaaataa 121722
CP 1108 CACTCCAGCCTGGGTGACAGAGTGAGACCTGTCAAAAAA 1059

RESULT 9
ID HSAB1901 standard; DNA; HMW; 8339 BP.
AC AB001901;
NI d1112091
DT 26-JUL-1997 (Rel. 52, Created)
DT 26-JUL-1997 (Rel. 52, Last updated, Version 1)
DE Homo sapiens PACE4 gene, exon 4-7.
DE alternative splicing; PACE4.
OC Eukaryotes; mitochondrial eukaryotes; Metazoa; Chordata;
OC Eukaryotes; mitochondria; Eutheria; Primates; Catarrhini; Homnidae;
OC Vertebrata; Mammalia; Eutheria; Primates; Catarrhini; Homnidae;
OC Homo.
RN [1]
RP 1-8339
RA Matsuda Y.;
RT Submitted (14-MAR-1997) to the EMBL/GenBank/DBJ databases.
RL Yoshiko Matsuda, The University of Tokushima, Department of
RL Biological Science and Technology; Minamijosanjima-cho 2-1,
RL Tokushima, Tokushima 770, Japan
RL (E-mail:matsuda@bio.tokushima-u.ac.jp, Tel:0886-56-7523,
RL Fax:0886-55-3161)
RN [2]
RA Tsuji A., Hine C., Tamai Y., Yonemoto K., Mori K., Yoshida S.,
RA Bando M., Mori K., Akamatsu T., Matsuda Y.;
RT Genomic organization and alternative splicing of human PACE4
RT (SPC4), kexin-like processing endoprotease";
RL J. Biochem. 122:438-452(1997).
FH key Location/Qualifiers
FH source 1..8339
FH /organism="Homo sapiens"

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FT /number=7
SQ Sequence 8339 BP; 1979 A; 2062 C; 2033 G; 2240 T; 25 other;

Query Match 8.8%; Score 124; DB 8; Length 8339;
Best Local Similarity 79.6%; Pred. No. 2.60e-64;
Matches 187; Conservative 0; Mismatches 45; Indels 3; Gaps 3;

Db 261 ttttttttttttgacagagctctgctgtgttgcacagactgagtgagtgacacacat 320
QY 1062 TTTTGTGTTTGTGACAGGCTCTCAGCTGTCCACAGGCTGGAGTGCAGTGGCACCAC- 1120
Db 321 catggtcactgagccttacttccag-gctcaagcaatccttcaactcagctcct 379
QY 1121 CATGGCTCTGCAAGCCTTACCTGTGGAGCTCAAGTGAATCCTGCTCAATCTCT 1180
Db 380 gagagcttgagactacagagatgcacatcatgccagctagattttttttttt 439
QY 1181 -AGTAGCTGGAAGTACAGAGAGAGGCGCACACACACCTGACTTTTGTGTTTGT 1239
Db 440 tggagaggtgggtttcaccatgttgcacagctgtgtcctcaactcctggctca 494
QY 1240 GGTAAAGATGACATTTCGCGCATGTTGTACAGGCTGGTCAAACTCCTAGTTCA 1294

RESULT 10
LOCUS HUMHDC 32351 bp DNA PRI 10-JUN-1994
DEFINITION Human gene for L-histidine decarboxylase, complete cds.
ACCESSION D16583
NID 9516770
KEYWORDS L-histidine decarboxylase.
SOURCE Homo sapiens DNA, clones lambda HDC[1, 2, 3 and 4].
ORGANISM Homo sapiens
Eukaryotes; mitochondrial eukaryotes; Metazoa; Chordata;
Vertebrata; Mammalia; Eutheria; Primates; Catarrhini; Homnidae;
Homo.
REFERENCE
1 (sites)
Yatsunami,K., Ohtsu,H., Tsuchikawa,M., Higuchi,T., Ishibashi,K.,
Shida,A., Shima,Y., Nakagawa,S., Yamauchi,K., Yamamoto,M.,
Hayashi,N., Matanabe,T. and Ichikawa,R.
Structure of the L-histidine decarboxylase gene
J Biol. Chem. 269 (2), 1554-1559 (1994)
MEDLINE 94117478
REFERENCE
2 (bases 1 to 32351)
Yatsunami,K.
JOURNAL Unpublished (1993)
REFERENCE
3 (bases 1 to 32351)
Yatsunami,K.
TITLE Direct Submission
COMMENT Submitted (02-JUL-1993) to the DDBJ/EMBL/GenBank databases. Kimio
Yatsunami, Japan Tobacco INC., Pharmaceutical Basic Research Lab.;
1-13-2 Fukuura Kanazawa-ku, Yokohama, Kanagawa 236, Japan
(Tel:045-786-7690(ex.3390), Fax:045-786-7692)
Submitted (02-JUL-1993) to DDBJ by:
Kimio Yatsunami
Dept. of Pharmaceutical
Basic Research Lab
Japan Tobacco INC.
1-13-2 Fukuura, Kanazawa-ku
Yokohama, Kanagawa 236
Japan
Phone: 045-786-7690 x3390

```

FEATURES Fax: 045-786-7692.
Location/Qualifiers
source 1..32351
/organism="Homo sapiens"
/clone_11b="EMBL3"
protein_bind 5447..5452
/bound_moiety="GATA binding protein"
protein_bind 5460..5464
/bound_moiety="LBP-1 (leader-binding protein-1)"
misc_signal 5592..5597
/note="CAC box"
misc_signal 5733..5738
/note="CAC box"
misc_signal 6124..6129
/note="CAC box"
protein_bind 6551..6555
/bound_moiety="LBP-1"
protein_bind 6788..6793
/bound_moiety="GATA binding protein"
protein_bind 6826..6831
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protein_bind 6895..6900
/bound_moiety="GATA binding protein"
protein_bind 6965..6969
/bound_moiety="LBP-1"
protein_bind 7169..7173
/bound_moiety="LBP-1"
protein_bind 7183..7188
/note="CAC box"
GC_signal 7221..7226
TATA_signal 7252..7259
/note="TATA-like sequence"
protein_bind 7268..7272
/bound_moiety="LBP-1"
exon 7278..7414
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/number=1
/bound_moiety="LBP-1"
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join(7384..7414,9600..9772,14491..14604,15461..15583,
18247..18381,18638..18781,19245..19311,20137..20299,
20391..20481,24567..24665,29671..29772,29907..30653)
/EC_number="4.1.1.22"
/codon_start=1
/product="L-histidine decarboxylase"
/db_xref="PID:d1004531"
/db_xref="PID:g516771"
/translation="MMPEERYRGRGEMVDYICQYLSYRERRVTPDVOGYLRAOLP
ESAPEDPDSDSIFGDIERIIMPVVWSPHAYPALISPSILGMDALINCL
GFWASDPACTELFMVMDLAKMLGPEHLHHSSOGGVLOSSTVRESSTIALLA
ARKNKILEKTSERPDNDESCLNARLYAYASDOHSSVERKGLISLVKMEFLPVDNFS
LRREALQKALIEEDKQGLVFEVFCATLGTGVCALFDCLSLGPICAREGLMLIDNAY
AGTAFLCPEFRGLKGLIEYADSTFNPSSKMMVHPCDGFVWVKYKLOQTESVNIY
LRNANGVATDFMHWQIPLSRPVSVMVIVISFGKNQAHVHGTETAKFESELY
RNDSPFEIPAKRHGLVLEFRKGNCLTENVLKEIKAGRLFLIPATIDOKLIRRTV
TSGFTRDDILRDMNLIRDAATLILSOHCSPSPVGNLISIRARMACTSIQS
VSGAGDPYQARKITIKOPQVAGKPMKRENGLETLDPVDCSEENAPDATKHLIS
SELESTLYQTKRKIVRSLSNSVPSAOKPLTEASVXNGSSRVRIRPEEDMM
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/codon_start=1
intron 9773..14490
/number=2
exon 14491..14604
/codon_start=1
intron 14605..15460
/number=3
exon 15461..15583
/codon_start=1

intron /number=4
15584..18246
/number=4
exon 18247..18381
/codon_start=1
intron 18382..18637
/number=5
exon 18638..18781
/codon_start=1
intron 18782..19244
/number=6
exon 19245..19311
/codon_start=1
intron 19312..20136
/number=7
exon 20137..20299
/codon_start=1
intron 20300..20390
/number=8
exon 20391..20481
/codon_start=1
intron 20482..24566
/number=9
exon 24567..24665
/codon_start=1
intron 24666..29670
/number=10
exon 29671..29772
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intron 29773..29906
/number=11
exon 29907..30962
/codon_start=1
intron 30963..32351
/number=12

BASE COUNT 8594 a 7026 c 7405 g 9326 t

ORIGIN

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Best Local Similarity 75.7%; Pred. No. 4.87e-65;
Matches 206; Conservative 0; Mismatches 63; Indels 3; Gaps 3;

Db 17093 accattatctttttaaacaaggcctgttctgtctcccaaggctgagtgagtg 17152
QY 1054 ACCACTTTTCTTTTCTTTTGAAGGGTCTACTCTGTACCCAGGCTGAGTGAAGTG 1113

Db 17153 gaagcatcatgctcctgagcctcatctcctg-gcccaagcaatcctcaacctca 17211
QY 1114 GCACACACAGGCTCTCTGAGCCTTGACCTCGGAGAGCTCAAGTATCTCTGCTCA 1173

Db 17212 gctcccaagctgagctgagctcaggtgctgacactacacctgagctttgtttttgt 17271
QY 1174 GCTCCTTA-GTACTGGAAGTCAAGAGGAGGACACACACTGACTACTTTTGT 1232

Db 17272 tttttttg-tagaagacaggtctcactatgtgtccagagctggtcctaactcctgagct 17330
QY 1233 TTTGTTGGTAAAGATGGCATTTTCGCATGTTGTACAGGCTGCTCAAACTCTAGGTT 1292

Db 17331 caaggatcctcccaagctcgtgagttacag 17362
QY 1293 CACTTGGCTCCCAAGTGTGGAATTACAG 1324

RESULT 11 HSAC000012 100000 bp DNA HTG 03-OCT-1996
LOCUS *** SEQUENCING IN PROGRESS *** EPM1/APECED region of chromosome 21,
DEFINITION BAC clone B17J3; HTS phase 1, 13 unordered pieces.


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CC length 67458 69665: gap of unknown length * 69666 81215: contig  
CC of 11550 bp in length * 81216 83423: gap of unknown length * 83424  
CC 1000000: contig of 16577 bp in length.  
FH Key Location/Qualifiers  
FH source 1..100000  
FT /organism="Homo sapiens"  
FT FT /clone=="B17313"  
FT FT /clone_lib="Caltech/Research Genetics Whole-Genome BAC  
FT library"  
FT /note=""Sequence data collected from 3kb subclones  
FT (vector-puf5 (J.-B. Fan, Stanford Human Genome Center))  
FT using a transposon-mediated approach."  
SQ Sequence 100000 BP; 16988 A; 18331 C; 19442 G; 18704 T; 2635 other;  
  
Query Match 8.8%; Score 125; DB 5; Length 100000;  
Best Local Similarity 77.4%; Pred. No. 4,87e-65;  
Matches 219; Conservative 0; Mismatches 58; Indels 6; Gaps 5;  
  
Db 93847 ggcctggtgtgttgctcattccataatcccagcaactttggaggccgagtgaactca 93906  
1346 GCCCGGGCCTGGCAATTCATCTGTATCCACACACTTTGGGAGGCCAAAGTGAACTTA 1287  
CP 93907 gaagctttagacacagaccctggcgacaatgtgaagaocccgcttcac-aaa-aaatgcaa 93964  
1286 GGAGTTTAGACACAGCCTGTACAACATGGCCAAATGCCCATTTTACCACAAAACAAAAACAA 1227  
Db 93965 aaa--ttaagccaagcatgtgtgtgcacgcctctagtaaccaacttacttggaagcctgat 94022  
CP 1226 AAAAGTATGATCAGGAGTGCTGGCCCTTCTGTATTGTTCCACTACTAAG-AGAAGTGAAGC 1168  
Db 94023 ggagagatcaccttgagc-ccccaaagtgtgaggttcagttgagttgagatcacccactgc 94081  
CP 1167 AGAGAGATCACTTGAGCTCCACAGAGGTCAAAGCTGCAGAGAGCCATGGTGTGCTCACTGC 1108  
Db 94082 accccaagccttgtgtacagagcagcagacctctccaaaaaaa 94124  
CP 1107 ACTCCAGCCTTGCTGACAGAGTGAAGACCTCTCAAAAAAAAA 1065  
  
RESULT 13  
ID HS39A18 standard; DNA; HTG; 145194 BP.  
AC Z97054;  
NI e1053532  
DT 20-JUN-1997 (Rel. 52, Created)  
DT 20-JUN-1997 (Rel. 52, Last updated, Version 1)  
DE Human DNA sequence *** SEQUENCING IN PROGRESS *** from clone 339A18  
KW HTG, PHASEL.  
KW Homo sapiens (human)  
OC Eukaryota; mitochondria eukaryotes; Metazoa; Chordata;  
OC Vertebrata; Eutheraia; Primates; Catarrhini; Hominiidae; Homo.  
RN [1]  
RP 1-145194  
RA Yaudin M.;  
RT ;  
RL Submitted (06-NOV-1996) to the EMBL/GenBank/DDBJ databases.  
WL Wellcome Trust Genome Campus, Hinxton, Cambridgeshire, CB10 1SA,  
UK. E-mail enquiries: humgen@esanger.ac.uk Clone requests:  
CL clonerequests@esanger.ac.uk  
CC IMPOREANT: This sequence is unfinished and does not necessarily  
CC represent the correct sequence. Work on the sequence is in progress  
CC and  
CC the release of this data is based on the understanding that the  
CC sequence may change as work continues. The sequence may be  
CC contaminated  
CC with foreign sequence from E.coli, yeast, vector, phage etc.  
CC Order of segments is not known; 800 n's separate segments.  
CC Unfinished sequence: dU339A18 Contig_ID: 01495 Length: 13468 bp  
CC Unfinished sequence: dU339A18 Contig_ID: 01275 Length: 1181 bp  
CC Unfinished sequence: dU339A18 Contig_ID: 01198 Length: 1123 bp  
CC Unfinished sequence: dU339A18 Contig_ID: 01197 Length: 6108 bp  
CC Unfinished sequence: dU339A18 Contig_ID: 01258 Length: 1692 bp  
CC Unfinished sequence: dU339A18 Contig_ID: 01052 Length: 2161 bp
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CC	Unfinished sequence: dJ339A18	Contig_ID: 01494	Length: 3769 bp
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CC	Unfinished sequence: dJ339A18	Contig_ID: 00001	Length: 1048 bp
CC	Unfinished sequence: dJ339A18	Contig_ID: 00109	Length: 2530 bp
CC	Unfinished sequence: dJ339A18	Contig_ID: 00484	Length: 2883 bp
CC	Unfinished sequence: dJ339A18	Contig_ID: 01239	Length: 3632 bp
CC	Unfinished sequence: dJ339A18	Contig_ID: 00606	Length: 11527 bp
CC	Unfinished sequence: dJ339A18	Contig_ID: 00901	Length: 7102 bp
CC	Unfinished sequence: dJ339A18	Contig_ID: 01439	Length: 7531 bp
CC	Unfinished sequence: dJ339A18	Contig_ID: 00784	Length: 6928 bp
CC	Unfinished sequence: dJ339A18	Contig_ID: 00591	Length: 5877 bp
CC	Unfinished sequence: dJ339A18	Contig_ID: 00397	Length: 14465 bp
CC	Unfinished sequence: dJ339A18	Contig_ID: 00464	Length: 3758 bp
CC	Unfinished sequence: dJ339A18	Contig_ID: 01041	Length: 1591 bp
CC	Unfinished sequence: dJ339A18	Contig_ID: 00635	Length: 997 bp
CC	Unfinished sequence: dJ339A18	Contig_ID: 01314	Length: 7100 bp
FF	Key	Location/Qualifiers	
FF	source	1..145194	
FF	/organism="Homo sapiens"		
FF	/clone="339A18"		
FF	/chromosome="X"		
SQ	Sequence 145194 BP; 35039 A; 29424 C; 28997 G; 33165 T; 18569 other;		
	Query Match	8.8%; Score 124; DB 5; Length 145194;	
	Best Local Similarity 79.3%; Pred. No. 2,60e-64;		
	Matches 195; Conservative 0; Mismatches 47; Indels 4; Gaps 3;		
Db	40551 tgaaccagcagcttgagaccagcctctgggaacatgcaaaacccatctctacaaaaa	40610	
Cp	1294 TGAACCTTGAGATTGACACACGCTGTACAAACATGCGGAATGCCATCTTACCAACA	1235	
Db	40611 taaaaataaaaaaattgtgccagcgcgctgtgagcgcgacccctgtagtctcagctacttgg	40670	
Cp	1234 --AAAAACAAAATAATGTGTCAGGTGTGTGTGCTCTTCTGTATCTTCACGCTATAGG-	1178	
Db	40671 aggcctgagctgggaagatctgtctggc-gc-aaggtgaagagattgcagtgaccatgac	40729	
Cp	1177 AGACTGAGGAGGAGAGATCATTAGCTCCAGAGAGTCAAGGCTTCAGAGACCATGTGTG	1118	
Db	40730 atgcacatgcacatccagcctcttgacagagatgagaccctgtctcaaaaaaaaaaaaa	40789	
Cp	1117 GGCACATGCATCTCCAGCTGGGTGACAGAGAGAGACCCCTGTCAAAAAAATAAAG	1058	
Db	40790 agttgc 40795		
Cp	1057 TGTGTG 1052		
LOCUS	14		
DEFINITION	HS339A18 145194 bp DNA	HTG	20-JUN-1997
ACCESSION	Human DNA sequence *** SEQUENCING IN PROGRESS *** from clone		
NID	339A18; HTGS phase 1.		
KEYWORDS	g2213437		
SOURCE	HTG: HTGS_PHASE1.		
ORGANISM	human.		
REFERENCE	Homo sapiens		
AUTHORS	Eukaryotes; mitochondrial eukaryotes; Metazoa; Chordata;		
TITLE	Vertebrata; Mammalia; Eutheria; Primates; Catarrhini; Homiidae;		
JOURNAL	Homo.		
COMMENT	1 (bases 1 to 145194)		
	Vaudin,M.		
	Direct Submission		
	Submitted (06-NOV-1996) Wellcome Trust Genome Campus, Hinxton,		
	Cambridgeshire, CB10 1SA, UK. E-mail enquiries:		
	humangy@anger.ac.uk Clone requests: clonerequest@anger.ac.uk		
	IMPORTANT: This sequence is unfinished and does not necessarily		
	represent the correct sequence. Work on the sequence is in progress		
	and		

contaminated with foreign sequence from E.coli, yeast, vector, phage etc. Order of segments is not known; 800 n's separate segments. Unfinished sequence: d3339A18 Contig_ID: 01495 Length: 13468 bp Unfinished sequence: d3339A18 Contig_ID: 01275 Length: 1181 bp Unfinished sequence: d3339A18 Contig_ID: 01198 Length: 1123 bp Unfinished sequence: d3339A18 Contig_ID: 01197 Length: 6108 bp Unfinished sequence: d3339A18 Contig_ID: 01258 Length: 1692 bp Unfinished sequence: d3339A18 Contig_ID: 01052 Length: 2161 bp Unfinished sequence: d3339A18 Contig_ID: 01494 Length: 3769 bp Unfinished sequence: d3339A18 Contig_ID: 00286 Length: 868 bp Unfinished sequence: d3339A18 Contig_ID: 00001 Length: 1048 bp Unfinished sequence: d3339A18 Contig_ID: 00109 Length: 2530 bp Unfinished sequence: d3339A18 Contig_ID: 00484 Length: 2883 bp Unfinished sequence: d3339A18 Contig_ID: 01239 Length: 3632 bp Unfinished sequence: d3339A18 Contig_ID: 00606 Length: 11527 bp Unfinished sequence: d3339A18 Contig_ID: 00901 Length: 7102 bp Unfinished sequence: d3339A18 Contig_ID: 01439 Length: 7531 bp Unfinished sequence: d3339A18 Contig_ID: 00784 Length: 6928 bp Unfinished sequence: d3339A18 Contig_ID: 00051 Length: 5877 bp Unfinished sequence: d3339A18 Contig_ID: 00397 Length: 15570 bp Unfinished sequence: d3339A18 Contig_ID: 00464 Length: 5758 bp Unfinished sequence: d3339A18 Contig_ID: 01041 Length: 1885 bp Unfinished sequence: d3339A18 Contig_ID: 00834 Length: 1591 bp Unfinished sequence: d3339A18 Contig_ID: 00635 Length: 997 bp Unfinished sequence: d3339A18 Contig_ID: 01314 Length: 7100 bp.

*** WARNING: Phase 1 High Throughput Genome Sequence ***
 *** This sequence is unfinished. When sequencing is complete,
 * the sequence data presented in this record will be replaced
 * by a single finished sequence with the same accession number.

FEATURES
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 /organism="Homo sapiens"
 /clone="339A18"
 /chromosome="X"

BASE COUNT 35039 a 29424 c 28997 g 33165 t 18569 others

ORIGIN

Query Match 8.8%, Score 124, DB 128, Length 145194;
 Best Local Similarity 79.3%, Pred. No. 2.60e-64;
 Matches 195; Conservative 0; Mismatches 47; Indels 4; Gaps 3;

Db 40551 tgaaccagcagcttcgagccagccttggaacatgcaaacaccatctacaaaaa 40610
 11294 TGAACCTAGGAGGTTGAGACCAAGCTGTACAAATGCGGAATGCCATCTTACCAACA 1235
 Db 40611 taaaaataaaaaagttagccaggtgtgtagcgtgcacccctgagttccagctactggg 40670
 1234 - -AAAAACAAAAGTTAGTACAGTGTGTTGGCTTCTTGTGTTCCAGCTAGG- 1178
 Cp 40671 aggcgtgagtggtgaggttcttgagc-ccagtgacgaggttgcagtcacatgac 40729
 1177 AGACTGAGGAGGAGGATCACTTGAAGCTCCAGAGGTCAGAGGTCATGGTG 1118
 Db 40730 atgcacatgacatccagcctgctgcagacagagtgagaccctgtctcctcaaaaaa 40789
 1117 GTGCGACTGACCTCCAGCTGGGTGACAGAGTGAAGACCCCTGTCAAAAAAAG 1058
 Cp 40790 agttgc 40795
 1057 TGGTGC 1052

RESULT 15
 LOCUS HSAC000118 96625 bp DNA PRI 31-JAN-1997
 DEFINITION Human BAC clone RG072E11 from 7q21-7q22, complete sequence.
 ACCESSION AC000118
 NID g1809227
 KEYWORDS HTG.

SOURCE human.
 ORGANISM Homo sapiens
 Eukaryote; mitochondrial eukaryotes; Metazoa; Chordata; Vertebrata; Eutheria; Primates; Catarrhini; Homnidae; Homo.
 REFERENCE 1 (bases 1 to 96625)
 AUTHORS Minx,P., Graves,T. and Biewald,T.
 TITLE The sequence of H. sapiens BAC clone RG072E11
 JOURNAL Unpublished (1997)
 REFERENCE 2 (bases 1 to 96625)
 AUTHORS Waterston,R.
 TITLE Direct Submission
 JOURNAL Submitted (31-JAN-1997)
 COMMENT Genome Sequencing Center
 Department of Genetics, Washington University
 St. Louis, MO 63108, USA
 http://genome.wustl.edu/gsc
 e-mail: saplensew@wustl.edu

NOTICE: This sequence may not represent the entire insert of this clone. It may be shorter because we only sequence overlapping sections once, or longer because we provide a small overlap between neighboring submissions.

This sequence was finished as follows unless otherwise noted:
 all regions were double stranded or sequenced with an alternate chemistry; an attempt was made to resolve all sequencing problems, such as compressions and repeats; all regions were covered by sequence from more than one subclone; and the assembly was confirmed by restriction digest.

SOURCE INFORMATION:
 This clone is from the first release of the human BAC library. The library contains cloned DNA from a human male fibroblast cell line 978SK. For references see: Shizuya et al., Proc. Natl. Acad. Sci. 89:8794-8797 (1992); Kim et al., Genomics 34:213-218 (1996).

VECTOR: pBELO
 Selection: chloramphenicol

NEIGHBORING SEQUENCE INFORMATION:
 The clone sequenced to the left is H_RG161K23, 200 bp overlap.
 Actual start of this clone is at base position 129619 of H_RG161K23; actual end is at 96625 of H_RG072E11

This clone contains the STS SWS1727.

FEATURES
 source
 1..96625
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 /chromosome="7"
 /clone="RG072E11"
 /clone_1id="CTTB-978SK-B"
 /map="7q21-7q22"
 922..994
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 936..1031
 /note="73% similarity to Human cosmid U15422 (NID:g642458)"
 943..1056
 /note="68% similarity to Human cosmid 249862 (NID:g1213360)"
 1026..1090
 /note="73% similarity to Human cosmid 274022 (NID:g140331)"
 1109..1159
 /note="76% similarity to Human cosmid 268339 (NID:g149521)"
 1477..1551
 /note="74% similarity to Human cosmid 273359 (NID:g1322150)"
 complement(1836..2027)
 /rpt_family="Alu"
 2209..2268
 /note="73% similarity to Human YAC U35072 (NID:g1016713)"

misc_feature 2366..2468 /note="72% similarity to Human VAC U35072 (NID:g1016713)"
repeat_region 6349..6637 /rpt_family="ALU"
repeat_region 6933..7243 /rpt_family="ALU"
misc_feature 7991..8064 /note="81% similarity to Human cosmid 275890 (NID:g1430781)"
misc_feature 7994..8059 /note="80% similarity to Human EST H48092 (NID:g924144)"
repeat_region /complement(8403..8695)
misc_feature 9580..9839 /rpt_family="ALU"
repeat_region /note="100% similarity to Human EST H71176 (NID:g1042992)"
misc_feature 9840..10133 /rpt_family="ALU"
repeat_region 10247..10327 /note="72% similarity to Human cosmid 273418 (NID:g1322398)"
repeat_region 10509..10799 /rpt_family="ALU"
repeat_region /complement(10816..10849)
misc_feature 12410..12465 /note="78% similarity to Human cosmid U70984 (NID:g1552538)"
repeat_region /complement(13607..13638)
repeat_region /rpt_family="L1"
repeat_region /complement(13847..14152)
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repeat_region /note="match to Human cosmid 254073 (NID:g974829)"
repeat_region /complement(14427..14695)
misc_feature 15000..15055 /rpt_family="ALU"
repeat_region /note="76% similarity to Human ABL gene U07561 (NID:g514262)"
repeat_region /complement(17612..17661)
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repeat_region /complement(17949..18216)
repeat_region /rpt_family="ALU"
repeat_region /complement(19222..19503)
repeat_region /rpt_family="L1"
repeat_region /complement(19511..19803)
repeat_region /rpt_family="ALU"
repeat_region /complement(20198..20908)
misc_feature 21018..21056 /rpt_family="L1"
repeat_region /note="87% similarity to Human cosmid 270280 (NID:g1237039)"
repeat_region 22180..22445 /rpt_family="MER"
misc_feature 22473..22548 /note="75% similarity to Human cosmid 268331 (NID:g147582)"
misc_feature 22483..22584 /note="82% similarity to Human cosmid U51281 (NID:g1256772)"
repeat_region /complement(23222..23515)
repeat_region /rpt_family="ALU"
repeat_region 24106..24377 /rpt_family="ALU"
repeat_region /rpt_family="ALU"
repeat_region 24597..24952 /note="match to Human EST M78483 (NID:g9272799)"
misc_feature 26387..26640 /rpt_family="THE"
misc_feature 26749..26862 /note="77% similarity to Human cosmid 275889 (NID:g1430780)"
misc_feature 26793..26836 /note="80% similarity to Human EST T51746 (NID:g553603)"
misc_feature 26808..26902

repeat_region /note="66082 (NID:g1519282)"
27108..27701 /rpt_family="ALU"
misc_feature 28087..28115 /note="89% similarity to Human PAC Z76735 (NID:g1438501)"
repeat_region 28391..28735 /rpt_family="MER"
misc_feature /complement(28966..29167)
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misc_feature /complement(29601..29652)
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29892..29918 /note="83% similarity to Human cosmid 273495 (NID:g1332499)"
misc_feature 30085..30121 /note="83% similarity to Human cosmid 273495 (NID:g1332499)"
misc_feature 30396..30928 /note="similar to Human clones U66082 (NID:g1519282) and U66083 (NID:g1519284)"
misc_feature 30462..30896 /note="70% similarity to Human EST W93033 (NID:g1422184)"
repeat_region /complement(31607..31884)
misc_feature 33037..33099 /rpt_family="ALU"
misc_feature /note="80% similarity to Human breakpoint cluster region gene U07000 (NID:g487344)"
33083..33205 /note="78% similarity to Human cosmid 268331 (NID:g147582)"
repeat_region /complement(33220..33509)
repeat_region /rpt_family="ALU"
repeat_region /complement(34518..34755)
repeat_region /rpt_family="ALU"
repeat_region /complement(35928..36215)
misc_feature 36996..37072 /note="76% similarity to Human cosmid 273359 (NID:g1322150)"
misc_feature 37029..37131 /note="75% similarity to Human EST H85739 (NID:g1067318)"
repeat_region 37195..37486 /rpt_family="ALU"
repeat_region 37815..37851 /rpt_family="L1"
repeat_region 37917..38018 /rpt_family="L1"
repeat_region 38047..38302 /rpt_family="L1"

...
Note: remainder of annotations omitted.

Query Match 8.6%; Score 121; DB 89; Length 96625;
Best Local Similarity 78.6%; Pred. No. 3.99e-22;
Matches 180; Conservative 0; Mismatches 47; Indels 2; Gaps 2;

Db 90537 gggagttgagaccagcctgggcaacatggtgaaacccgtctacttaaaatatyat 90596
|||||
Cp 1286 GGAATTGAGACACCGCTGTACCAATGCGGAATGCGATCTTACCAACAAAAACAA 1227
|||||
Db 90597 aaactagcctgagtggtggcacatgctgtagtcacacgtatctggagagctgggc 90656
|||||
Cp 1226 AAAAGTTAGTCAGGTGGTGCGCCCTTCTTGTAGTCCAGCTACTAGG-AGACTGAGGC 1168
|||||
Db 90657 acgaatccttgaac-caggaggaagaggtgacgtgacgtgacgaatgatccgtgc 90715
|||||
Cp 1167 AGAGAGATCACTGAGCTCCCAAGGCAAGGCTGCGAGAGACCATGCTGTGCTCCACTGC 1108
|||||
Db 90716 actccagcctgggtgacaaagcgagacccctgtctcaaaaaaaaaa 90764
|||||
Cp 1107 ACTCCAGCCTGGGAGACAGAGTGAACCTCTCAAAAAAAAAAAAAA 1059

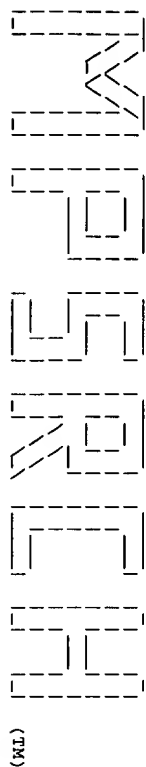
Thu Mar 26 09:16:03 1998

US-08-236-918A-7.rge

Page 13

Search completed: Wed Mar 25 13:28:43 1998
Job time : 1987 secs.

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Msrch_n n.a. - n.a. database search, using Smith-Waterman algorithm
Run on: Wed Mar 25 13:54:43 1998; MasPar time 384.28 Seconds
Output not generated. 928.964 Million cell updates/sec

Title: >US-08-236-918A-7
Description: (1-1415) from 5674704.seq
Perfect Score: 1415
N.A. Sequence: 1 AGTGGAAAGTCTCCGCGAG.....TGATAAAAA.....AAAAA 1415
Comp: TCACCTTCAAGAGCGCGTC.....ACTATTTT.....TTTTTTT

Scoring table: TABLE default
Gap 6

Nmatch STD : Dbase 0; Query 0

Searched: 333433 seqs, 126143548 bases x 2

Post-processing: Minimum Match 0%

Listing first 45 summaries

Database: STS
1:STS1 2:STS2 3:STS3 4:STS4 5:STS5 6:STS6 7:STS7 8:STS8
9:STS9 10:STS10 11:STS11 12:STS12 13:STS13 14:STS14
15:STS15 16:STS16 17:STS17 18:STS18 19:STS19
20:STS20 21:STS21 22:STS22 23:STS23 24:STS24
25:STS25 26:STS26 27:STS27 28:STS28 29:STS29
30:STS30 31:STS31 32:STS32 33:STS33 34:STS34
35:STS35 36:STS36 37:STS37 38:STS38 39:STS39
40:STS40 41:STS41 42:STS42 43:STS43 44:STS44
45:STS45 46:STS46 47:STS47 48:STS48 49:STS49
50:STS50 51:STS51 52:STS52 53:STS53 54:STS54
55:STS55 56:STS56 57:STS57 58:STS58 59:STS59
60:STS60 61:STS61 62:STS62 63:STS63 64:STS64
65:STS65 66:STS66 67:STS67 68:STS68 69:STS69
70:STS70 71:STS71 72:STS72 73:STS73 74:STS74
75:STS75 76:STS76 77:STS77 78:STS78 79:STS79
80:STS80 81:STS81 82:STS82 83:STS83 84:STS84
85:STS85 86:STS86 87:STS87 88:STS88 89:STS89
90:STS90 91:STS91 92:STS92 93:STS93 94:STS94
95:STS95 96:STS96

Statistics: Mean 12.191; Variance 5.851; scale 2.084

Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description	Pred. No.
1	1415	100.0	1415	9	G28572 human STS SHGC-35316.	0.00e+00
2	300	21.2	515	8	G26790 human STS STS_U03397.	1.78e-222

3	115	8.1	373	31	AA470779	ne19e10.s1	NC1_CGAP_C	3.32e-65
4	115	8.1	428	80	HSAA70779	ne19e10.s1	NC1_CGAP_P	3.32e-65
5	115	8.1	478	67	HS1285256	aa55b01.s1	NC1_CGAP_G	3.32e-65
6	115	8.1	428	30	AA488846	aa55b01.s1	NC1_CGAP_P	3.32e-65
7	114	8.1	503	52	HS1186885	at12d11.s1	NC1_CGAP_G	2.15e-64
8	114	8.1	503	22	AA282360	at12d11.s1	NC1_CGAP_G	2.15e-64
9	111	7.8	284	37	AA482730	nf47g04.s1	NC1_CGAP_A	5.84e-62
10	111	7.8	284	65	HS1274183	nf47g04.s1	NC1_CGAP_A	5.84e-62
11	109	7.7	323	66	HS1275688	ne88g02.s1	NC1_CGAP_K	2.42e-60
12	109	7.7	323	32	AA484267	ne88g02.s1	NC1_CGAP_P	2.42e-60
13	108	7.6	260	38	AA502565	ng62f10.s1	NC1_CGAP_L	1.56e-59
14	108	7.6	260	69	HS1298476	ng62f10.s1	NC1_CGAP_L	1.56e-59
15	108	7.6	300	20	AA262532	zs17c02.r1	NC1_CGAP_G	1.56e-59
16	108	7.6	300	76	HSAA62532	zs17c02.r1	NC1_CGAP_G	1.56e-59
17	108	7.6	338	68	HS1288482	aa46a10.s1	NC1_CGAP_P	1.56e-59
18	108	7.6	338	31	AA490845	aa46a10.s1	NC1_CGAP_P	1.56e-59
19	108	7.6	373	28	AA468271	nc76a08.r1	NC1_CGAP_P	1.56e-59
20	108	7.6	373	79	HSAA68271	nc76a08.r1	NC1_CGAP_P	1.56e-59
21	107	7.6	399	30	AA487199	ab19f01.s1	Stratagene	9.98e-59
22	107	7.6	399	67	HS1283006	ab19f01.s1	Stratagene	9.98e-59
23	108	7.6	447	76	HSAA27643	zn81e05.s1	Stratagene	1.56e-59
24	107	7.6	460	42	AA525018	nh36a12.s1	NC1_CGAP_P	9.98e-59
25	107	7.6	460	72	HS1316697	nh36a12.s1	NC1_CGAP_P	9.98e-59
26	106	7.5	328	71	HS1309371	ng70f10.s1	NC1_CGAP_P	6.38e-58
27	106	7.5	328	39	AA515733	ng70f10.s1	NC1_CGAP_P	6.38e-58
28	106	7.5	400	6	G16405	human STS SHGC-10228	4.07e-57	
29	105	7.4	328	28	AA469451	nc74c02.s1	NC1_CGAP_P	4.07e-57
30	105	7.4	328	63	HS1261499	nc74c02.s1	NC1_CGAP_P	4.07e-57
31	105	7.4	386	4	G09037	human STS CHIC ATT4B1	4.07e-57	
32	105	7.4	465	49	HS1145590	nc10h07.r1	NC1_CGAP_P	4.07e-57
33	105	7.4	465	25	AA426159	nc10h07.r1	NC1_CGAP_P	4.07e-57
34	104	7.3	341	24	AA468319	nc77a05.s1	NC1_CGAP_P	2.59e-56
35	104	7.3	341	79	HSAA68319	nc77a05.s1	NC1_CGAP_P	2.59e-56
36	104	7.3	361	49	HS1149379	nc37d05.s1	NC1_CGAP_P	2.59e-56
37	104	7.3	361	28	AA429986	nc37d05.s1	NC1_CGAP_P	2.59e-56
38	104	7.3	372	28	AA468388	nc76f10.s1	NC1_CGAP_P	2.59e-56
39	104	7.3	372	79	HSAA68388	nc76f10.s1	NC1_CGAP_P	2.59e-56
40	104	7.3	382	69	HS1298433	ng22f109.s1	NC1_CGAP_P	2.59e-56
41	104	7.3	382	38	AA502522	ng22f109.s1	NC1_CGAP_P	2.59e-56
42	104	7.3	430	79	AA468484	nc78d10.r1	NC1_CGAP_P	2.59e-56
43	104	7.3	430	28	HSAA68484	nc78d10.r1	NC1_CGAP_P	2.59e-56
44	104	7.3	486	43	AA528706	nf51e11.s1	NC1_CGAP_P	2.59e-56
45	104	7.3	486	73	HS1320180	nf51e11.s1	NC1_CGAP_P	2.59e-56

ALIGNMENTS

RESULT	1	G28572	1415 bp	DNA	STS	01-JUL-1996
LOCUS		human STS SHGC-35316.				
DEFINITION		human STS SHGC-35316.				
ACCESSION		G28572				
KEYWORDS		STS sequence; primer: sequence tagged site.				
ORGANISM		human.				
SOURCE		Homo sapiens				
REFERENCE		Eukaryotes: mitochondrial eukaryotes; Metazoa; Chordata;				
AUTHORS		Vertebrata; Euteria; Primates; Catarrhini; Homidae; Homo.				
JOURNAL		Myers, R.M.				
COMMENT		Unpublished (1996)				

Contact: Richard M. Myers
Stanford Human Genome Center (SHGC)
Stanford University School of Medicine
Department of Genetics, W-344, Stanford, CA 94305, USA
Tel: 4157259687
Fax: 4157259689
Email: myerseshgc.stanford.edu

Primer A: TGAATGGAAGTCAATAGGC
Primer B: AAAAAGTGTGCAATTTTAAAGC
STS size: 180
PCR Profile:

QY	1059	TTTTTTTTTTTTTTTGTACAGGGCTCAGCTCTGTACACCAGGCTGAGTGGTCAGTGGCAC	1118
Db	62	atcatggttaactgcagccttgaattctcggcgtcaagtgatctctcgtcctcaagcct	120
QY	1119	ACCAAGGCTCTCTCACCCTTGACCTCTGGAGACTCAATGATCCCTCAGCTCT-1177	
Db	121	ccccatggttgggaactcagaagaagcaaccaaccaaccagctcga-ttttatttttctt	179
QY	1178	CGTGTGCTGGAACTCAAGAGGAGGGCCACACACTACACAACTTTTGTGTTTTTGT	1237
Db	180	ttg-taaagcagagcttcgtctatgtttgatacagacttatattgaactcctggtt	233
QY	1238	TTGGTAAGATGCGATTTCGCCAGTGTGTACAGGCTGGTCTCAAACTCCTAAGTT	1292

RESULT	4
ID	HSA070779 standard; RNA; EST; 373 BP.

AC	AA470779;	
NI	g2198088	
DT	21-JUN-1997 (Rel. 52, Created)	
DE	28-JUN-1997 (Rel. 52, last updated, Version 3)	
CC	nel9el0.si NCI-CGAP_C03 Homo sapiens cDNA clone 881706 similar to	
CC	contains Alu repetitive element; contains element LTR10 repetitive	
CC	element ;.	
KM	EST.	
OS	Homo sapiens (human)	
OC	Eukaryotae; mitochondriall eukaryotes; Metazoa; Chordata;	
OC	Vertebrata; Mammalia; Eutheria; Primates; Catarrhini; Homnidae;	
OC	Homo.	
RN	[1]	
RP	1-373	
RA	NCI-CGAP;	
RT	"National Cancer Institute, Cancer Genome Anatomy Project (CGAP),	
RT	Tumor Gene Index";	
RL	Unpublished.	
CC	Contact: Robert Strausberg, Ph.D. Tel: (301) 496-1550 Email:	
CC	Robert.Strausberg@nih.gov Tissue Procurement: Elias Campo, M.D.,	
CC	Michael R. Emmert-Buck, M.D., Ph.D. CDNA Library Preparation: M.	
CC	Berto Soares, Ph.D. CDNA Library Arrayed by: Greg Lennon, Ph.D. D.	
CC	Sequencing by: Washington University Genome Sequencing Center Clo	
CC	distribution: NCI-CGAP clone distribution information can be foun	
CC	through the I.M.A.G.E. Consortium/LINL at:	
CC	www.bio.11n1.gov/dbnp/image/image.html Insert Length: 1322 Str	
CC	Error: 0.00 Seq primer: -41m13 fwd. ET from Amersham High quality	
CC	sequence stop: 359.	
RH	Key	Location/Qualifiers

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FT      SOURCE
FT      1..373
FT      /organism="Homo sapiens"
FT      /note="Vector: p773D-Pac (Pharmacia) with a modified
FT      polylinker; Site_1: Not I; Site_2: Eco RI; 1st strand cDNA
FT      was prepared from 12 pooled bulk tumor samples and primed
FT      with a Not I - oligo(dT) primer. Double-stranded cDNA was
FT      ligated to Eco RIadaptors (Pharmacia), digested with Not I
FT      and cloned into the Not I and Eco RI sites of the modified
FT      p773J vector. Library went through one round of
FT      normalization."
FT      /clone="881706"
FT      /clone_lib="NCI_CGAP_Cc3"
FT      /sex="pooled"
FT      /tissue_type="colon"
FT      /lab_host="DH10B"
FT      mRNA
FT      <1..>373
FT      Sequence 373 BP; 90 A; 89 C; 88 G; 106 T; 0 other;
FT      30

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Query Match	8.18;	Score 115;	DB 80;	Length 373;
Best Local Similarity	78.78;	Pred. No. 3.32e-65;		
Matches	185;	Conservative	0;	Mismatches 46;
				Indels 4;
				Gaps 4

```
D8      2 ttttcttttttgagacagggtcactctgttacctaagtgcggaatggcaaca    61
        |||||
QY     1059 ttttttttttttttttttttttcaccctgatcccgcatgccattggcacccc   1118
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Db 62 atcatggttcaacgcagcccttgatattccgg -gtcaatgatcttctgcctcaagcct 120
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 QY 1119 ACCATGGCCTCTGACACCTTGACCTCTGGAGACTCAATGATCCCTCGCTCAGCTC 1177
 |||||
 Db 121 cccagtatggtggactacagaagaagcaccacacccagcga -ttttattttctt 179
 |||||
 QY 1178 CCTAGTAGCTGGAACTCAAGGAAGGCCCCACCACTGACAACTTTTTTTTGGT 1237
 |||||
 Db 180 ttg-taaagcagagctctgactatgtttgaatcaagcctatttgaactccctggct 233
 |||||
 QY 1238 TTGGTAAGATGACGATTGGCCCATGTTGTACAGGCTGGTCTCAAACTCTTAAGTT 1292
 |||||

RESULT	5
ID	HS1285256 standard; RNA; EST; 428 BP.

AC AA488846;
NI g2218448
DT 01-JUL-1997 (Rel. 52, Created)
DT 01-JUL-1997 (Rel. 52, Last updated, Version 1)
DE aa55b01.st NC1:CGAP-CGB1 Homo sapiens cDNA clone 824809 3' similar
DE to contains Alu repetitive element;.
KW EST.
OS Homo sapiens (human)
OC Eukaryotae; mitochondriale eukaryotes; Metazoa; Chordata;
OC Vertebrata; Mammalia; Eutheria; Primates; Catarrhini; Hominiidae;
OC Homo.
RN [1]
RP 1-428
RA NC1-CGAP;
RT "National Cancer Institute, Cancer Genome Anatomy Project (CGAP),
RT Tumor Gene Index";
RL Unpublished.
CC Contact: Robert Strausberg, Ph.D. Tel: (301) 496-1550 Email:
CC Robert.Strausberg@nih.gov Tissue Procurement: Louis M. Staudt,
CC M.D., Ph.D., David Allman, Ph.D., Gerald Marti, M.D. cDNA Library
CC Preparation: M. Bento Soares, Ph.D., M. Fatima Bonaldo, Ph.D. cDNA
CC Library Arrayed by: Greg Lennon, Ph.D. DNA Sequencing by:
CC Washington University Genome Sequencing Center Clone Distribution::
CC NC1-CGAP clone distribution information can be found through the
CC I.M.A.G.E Consortium/LLNL at:
CC www-bio.llnl.gov/bdpr/image/image.html Seq primer: -41m3 fwd. ET
CC from Amersham High quality sequence stop: 418.
KH Key Location/Qualifiers

FT	source	1..428
FT		/organism="Homo sapiens"
FT		/note="Vector: pT73D-Pac (Pharmacia) with a modified
FT		polylinker. Site_1: Not I; Site_2: Eco RI; 1st strand cDNA
FT		was prepared from human tonsillar cells enriched for
FT		germinal center B cells by flow sorting (CD20+, IgD-),
FT		provided by Dr. Louis M. Staudt (NCI). Dr. David Altman
FT		(NCI) and Dr. Gerald Marti (CBER). cDNA synthesis was
FT		primed with a Not I - oligo(dT) primer
FT		[5'-TGTTACCACATCTGAAGTGGAGGGCCGCTCATTTTTTTTTTTTTT-3'].
FT		Double-stranded cDNA was ligated to Eco RI adaptors (
FT		Pharmacia), digested with Not I and cloned into the Not I
FT		and Eco RI sites of the modified pT73 vector. Library was
FT		
+		
FT		through one round of normalization, and was constructed by
FT		Bento Soares and M. Fatima Bonaldo."
FT		/clone="824809"
FT		/clone_1lb="NCI CGAP GCBI"
FT		/tissue_type="germinal center B cell"
FT		/lab_host="DH10B"
FT		complement(<1..>428)
FT	mrna	
FT	Sequence	428 BP; 109 A; 106 C; 91 G; 122 T; 0 other;
+		

Query Match	8.1%;	Score 115;	DB 67;	Length 428;
Best Local Similarity	78.2%;	Pred. No. 3.32e-65;		
Matches 187;	Conservative	0;	Mismatches 48;	Indels 4;
			Gaps	4;

Db 2 ttttttttttttgagatgagggtctcacctctgtcacccagactggaattgcagctgtgc 61
|||||

Query Match 8.1%; Score 115; DB 30; Length 428;

Query	1059	TTTTTTTTTTTTTTTTTTGACAGGGTCTACACTC- GTACACCCAGGCTGGAGTGCAGTGGCAGC	1117
Db	62	aatacaactcactctgtgcttgcgttctctg-gctcaagaagatctcccaactaagcct	120
Oy	1118	CACCAAGTCTCTCTCTCACCCTTGACCTCTGGAGCTCAAGATGATCTCTCTGCTAGTCT	1177
Db	121	cctgtatgctgtggagactaacgtaagtgtggccaccacacccggcgaattatgttcatc	180
Oy	1178	CCT-AGTAGCTGTGAACTACAAAGAG-GGCCACCCACCTGACTACTTTTGTGTTTTT	1235
Db	181	tttttcagagacgggggtttccacatgtgtcccaagctcgtgtcacaactcctgggctca	239
Oy	1236	GTTTGTAAAGATGCATTTCCGATGTTGTACAGGCTGGTCTCAAACTCTAGAGTTCA	1294
RESULT	6		
LOCUS	AA488846	428 bp	EST
DEFINITION	aa55b01.s1 NCI-CGAP-GC81 Homo sapiens cDNA clone 824809 3' similar to contains Alu repetitive element;	25-JUN-1997	
ACCESSION	AA488846		
VERSION	g2218448		
ORIGIN	EST.		
SOURCE	human.		
ORGANISM	Homo sapiens		
REFERENCE	Vertebrate; mitochondrial eukaryotes; Metazoa; Chordata; Eutheria; Mammalia; Eutheria; Primates; Catarrhini; Homiidae;		
AUTHORS	Homo.		
TITLE	1 (bases 1 to 428)		
JOURNAL	NCI-CGAP.		
COMMENT	National Cancer Institute, Cancer Genome Anatomy Project (CGAP), Tumor Gene Index Unpublished (1997)		
CONTACT	Contact: Robert Strausberg, Ph.D.		
TELEPHONE	Tel: (301) 496-1550		
EMAIL	Email: Robert.Strausberg@nih.gov		
TISSUE	Tissue Procurement: Louis M. Staudt, M.D., Ph.D., David Allman, Ph.D., Gerald Marti, M.D.		
CDNA	cDNA Library Preparation: M. Bento Soares, Ph.D., M. Fatima Bonaldo, Ph.D.		
CEN	cDNA Library Arrayed by: Greg Lennon, Ph.D.		
CLONE	DNA Sequencing by: Washington University Genome Sequencing Center		
CLONE	clone distribution: NCI-CGAP clone distribution information can be found through the I.M.A.G.E. Consortium/LLNL at: www-bio.llnl.gov/bdnp/image/image.html		
PRIMER	Seq primer: -41ml3 fwd. ET from Amersham		
QUALITY	High quality sequence stop: 418.		
LOCATION	Location/Qualifiers		
ORGANISM	1..428		
NOTE	/organism="Homo sapiens"		
NOTE	/note="Vector: pRT3D-Pac (Pharmacia) with a modified polylinker; Site_1: Not I; Site_2: Eco RI; 1st strand cDNA was prepared from human tonsillar cells enriched for germinal center B cells by flow sorting (CD20+, IgD-), provided by Dr. Louis M. Staudt (NCI), Dr. David Allman (NCI) and Dr. Gerald Marti (CBER). cDNA synthesis was primed with a Not I - oligo(dT) primer		
NOTE	[5'-TGTTACCAATCTCAAGTGGAGCGCGCCCTCATTTTTTTTTTTTTTTT-3'] Double-stranded cDNA was ligated to Eco RI adaptors (Pharmacia), digested with Not I and cloned into the Not I and Eco RI sites of the modified pRT3D vector. Library went through one round of normalization, and was constructed by Bento Soares and M. Fatima Bonaldo.		
NOTE	/clone="824809"		
NOTE	/clone-lib="NCI-CGAP-GC81"		
NOTE	/tissue_type="germinal center B cell"		
NOTE	/lab_host="DH10B"		
NOTE	complement(<1..>428)		
BASE	109 a	106 c	122 t
ORIGIN			

Best Local Similarity 78.2%; Pred.No. 3,326-65;
Matches 187; Conservative 0; Mismatches 48; Indels 4; Gaps 4;

Db 2 ttttcttttttttgagatcgggttcacattctgcccaccgaactggagtgcagtgatgc 61
|||||
Oy 1059 TTTTCTTTTTTTTTTGACAGGGGTCTCACTCT-GTCACCACCGAGGCGATCAGTGCAC 1117

Db 62 aatacaactcacitctgcttcggttccttg-gtctaagaatctccacactcagct 120
||| |||||
Oy 1118 CACCATGGCTCTCTGACACCTTGACTCTGGAGGTCAAAGTATCTCTGCTGATGCT 1177

Db 121 cctgatgctcgaggactacaactatgtagccacacacgggccaattatctgatttc 180
||| |||||
Oy 1178 CCT-AGTAGCTGAAGACTACAAGGAAG-GGCCACACACACTGACTAATTGTTTTTTT 1235

Db 181 tttttcagagacgggtttaccatgtgtgccacagcttgtctaaactcctggctca 239
||| |||||
Oy 1236 GTTTGTAAAGATGCAATTTCGCACTGTTGTACAGGGCTGCTCAAACTCCTAGGTTCA 1294

RESULT 7
ID HS1186885 standard; RNA; EST; 503 BP.
AC AA822360;
NI g1925276
DT 04-APR-1997 (Rel. 51, Created)
DT 20-JUN-1997 (Rel. 52, Last updated, Version 3)
DE z112d11.r1 NCI_CGAP_GCB1 Homo sapiens cDNA clone 712917 5' similar
to contains Alu repetitive element;contains element PFR7 repetitive
element ;.
DE
EW EST.
OS Homo sapiens (human)
OC Eukaryotae; mitochondrial eukaryotes; Metazoa; Chordata;
OC Vertebrate; Eutheria; Primates; Catarrhini; Hominiidae; Homo.
RN [1]
RP 1-503
RA NCI-CGAP;
RT "National Cancer Institute, Cancer Genome Anatomy Project (CGAP),
Tumor Gene Index";
RL Unpublished.

CC Contact: Robert Strausberg, Ph.D. Tel: (301) 496-1550 Email:
Robert.Strausberg@nih.gov This clone is available royalty-free
through LNL ; contact the IMAGE Consortium (info@image.llnl.gov)
CC for further information. Seq primer: -28m13 rev2 ET from Amershams
CC High quality sequence stop: 483.
FH Key Location/Qualifiers
FT source
FT 1..503
FT /organism="Homo sapiens"
FT /note="Vector: pYT7D-Pac (Pharmacia) with a modified
polylinker; Site_1: Not I; Site_2: Eco RI; 1st strand cDNA
was prepared from human tonsillar cells enriched for
germlinal center B cells by flow sorting (CD20+, IgD+),
provided by Dr. Louis M.Staudt (NCI). Dr. David Allman
(NCI) and Dr. Gerald Marti (GBER). cDNA synthesis was
primed with a Not I - oligo(dT) primer
[5'-TGTTACCAATCTGAAGGGAGCGGCGGCTCATTTTCTTTTTTTTTT-
3'] Double-stranded cDNA was ligated to Eco RI adaptors (Clontech
Pharmacia), digested with Not I and cloned into the Not I
and Eco RI sites of the modified pYT7S vector. Library when
labeled with [³²P]dATP and amplified by PCR." FT
FT through one round of normalization, and was constructed by
FT Bento Soares and M. Fatima Bonaldo." FT
FT /clone="712917"
FT /clone_lib="NCI_CGAP_GCB1"
FT /tissue_type="germlinal center B cell"
FT /lab_host="DH10B"
FT <1...>503
SQ Sequence 503 BP; 138 A; 114 C; 146 G; 105 T; 0 other;

Query Match 8.1%; Score 114; DB 52; Length 503;
Best Local Similarity 76.3%; Pred. No. 2,156-64;
Matches 209; Conservative 0; Mismatches 59; Indels 6; Gaps 5;

LOCUS	AA823630	503 bp	mRNA	EST	13-JUN-1997
DEFINITION	z112d11.r1 NC1-CGAP-CG41 Homo sapiens cDNA clone 712917, 5' similar to contatans Alu repetitive element, contains element FTR7 repetitive element ;.				
ACCESSION	AA823630				
NID	91925276				
KEYWORDS	EST.				
SOURCE	human.				
ORGANISM	Homo sapiens				
	Eukaryotes; mitochondrial eukaryotes; Metazoa; Chordata; Vertebrata; Mammalia; Euthera; Primates; Catarrhini; Homnidae; Homo.				
REFERENCE	1 (bases 1 to 503)				
AUTHORS	NCI-CGAP.				
TITLE	National Cancer Institute, Cancer Genome Anatomy Project (CGAP), Tumor Gene Index				
JOURNAL	unpublished (1997)				
COMMENT					

1..503

/organism="Homo sapiens"
 /note="Vector: pT72D-pac (Pharmacia) with a modified
 polylinker: site_1: Not I; site_2: Eco RI; 1st strand cDNA
 was prepared from human tonsillar cells enriched for
 germinal center B cells by flow sorting (CD20+, Ig-),
 provided by Dr. Louis M. Staudt (NCI), Dr. David Allman
 (NCI) and Dr. Gerald Marti (CBER). cDNA synthesis was
 primed with a Not I - oligo(dG) primer
 15'-TGGTACCAATCTAGATGGAGCGCGCCATTTTCTTTTCTTTT
 3'). Double-stranded cDNA was ligated to Eco RI adaptors
 (Pharmacia), digested with Not I and cloned into the Not I
 and Eco RI sites of the modified pT72D vector. Library
 went through one round of normalization, and was
 constructed by Bento Soares and M. Fatima Bonaldo."
 /clone="71291"
 /clone_1lib="NCI_CGAP_GCB1"
 /tissue_type="germinal center B cell"
 /lab_host="DH10B"

mrna	<1..>503		
BASE COUNT	138 a	114 c	146 g 105 t
ORIGIN			

Query Match	8.18;	Score 114;	DB 22;	Length 503;
Best Local Similarity	76.38;	Pred. No. 2.15e-64;		

RESULT	9	AA482730	284 bp	mRNA	EST	09-JUL-1997
LOCUS		nt47504.s1	NCI-CGAP Alvl	Homo sapiens	CDNA clone	923094 similar to
DEFINITION		contains Alu repetitive element;.				
ACCESSION		AA482730				
NID		9221575				
KEYWORDS		EST.				
SOURCE		human.				
ORGANISM		Homo sapiens				
		Eukaryote; mitochondrial eukaryotes; Metazoa; Chordata;				
		Vertebrata; Mammalia; Eutheria; Primates; Carnivora; Homidae;				
		Homio.				
REFERENCE		1 (bases 1 to 284)				
AUTHORS		NCI-CGAP				
TITLE		National Cancer Institute, Cancer Genome Anatomy Project (CGAP),				
		Tumor Gene Index				
JOURNAL		Unpublished (1997)				

Contact: Robert Strausberg, Ph.D.
Tel: (301) 496-1550
Email: Robert_Strausberg@nih.gov
Tissue Procurement: Lee Helman, M.D., Michael R. Emmert-Buck, M.D., Ph.D.
CDNA Library Preparation: David B. Krizman, Ph.D.
CDNA Library Arrayed by: Greg Lennon, Ph.D.
DNA Sequencing by: Washington University Genome Sequencing Center
Clone distribution: NCI-CGAP clone distribution information can be found through the I.M.A.G.E. Consortium/LNL at: www.bio.llni.gov/dbirp/imagel/imagel.html

Insert Length: 379 Std Error: 0.00
Seq primer: -41m13 fwd. Et from Amersham

FEATURES

source

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/oranism="Homo sapiens"
/notes="Vector: pmp10; mRNA made from al
thabomyosarcoma, cDNA made by oligo-dr
non-directionally cloned. Size-selected
average insert size 600 bp. Reference:
(1996) Cancer Research 56:5380-5383."
/clonename="923094."
/clonelib="NCL-GAP Alvi"
/tissue="alveolar rhabdomyosarcoma"
/lab.host="DH10B"

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ORIGIN	BASE COUNT	97 a	71 c	72 g	44 t
mrna	<1..>284				

Query Match	7.8%;	Score 111;	DB 37;	length 284
Best Local Similarity	78.3%;	Pred. No. 5.84e-62;		

Matches	188;	Conservative	0;	Mismatches	47;	Indels	5;	Gaps	4;
Db	37	tgaaccaggaggttcgagaccagccctgggcaacatgycacaaatcccatctctacaacaaa						96	
Cp	1294	TGAACCTTAGGGATTGGAACACAGCTGTACACATATGGGAAATGCCATCTTTACCAACACA						1235	
Db	97	gaccacaaaaaaaatatagcttgggcatggtgtgacacacacctgtagtcoccagctactcag						156	
Cp	1234	-A-AAAAACAAAAGTAGTCAGGTGTGGTGGGCCCTTCCTTGTAGTTCACGCTACT-AG						1179	
Db	157	gaagccgagctcgggaagatacctaacttgaac-ccaaggaaggttcgaagcttgaagctgtgat						215	
Cp	1178	GAGACTGGAGCAGGAGGAGGTCACTTGAAGTCCCAAGGCAAGGGCTGGAGAGAGGCCATGCT						1119	
Db	216	tgcacccaatgcactccagaccctcgaagtaaacagagcaagaccgctatctcaaaaaaaaaaaaa						275	
Cp	1118	GGTGGCATCTGCACCTCCAGCCTTGGGTGAGACAGTAGAGACCCTGTCAAAAAAAAAAAAAAAA						1059	

PROCTIT 10
 HS1274183 standard; RNA; EST; 284 BP.

RESULT	10	standard; RNA; EST; 284 BP.
HS1274183		
AA482730:		
NI	92211575	
DT	24-JUN-1997	(Rel. 52, Created)
DT	10-JUL-1997	(Rel. 52, Last updated, Version 3)
DE	n147994.s1	NCI-CGAP-Alv1 Homo sapiens cDNA clone 923094 similar to
DE	contains	Alu repetitive element;.
KW	EST.	
OS	Homo sapiens (human)	
OC	Eukaryote; mitochondrial eukaryotes; Metazoa; Chordata;	
OC	Vertebrata; Mammalia; Eutheria; Primates; Catarrhini; Homnidae;	
OC	Homo.	
RP	[1]	
RP	1-284	
RA	NCI-CGAP;	
RT	"National Cancer Institute, Cancer Genome Anatomy Project (CGAP),	
RT	Tumor Gene Index";	
RL	unpublished.	
CC	Contact: Robert Strausberg, Ph.D. Tel: (301) 496-1550 Email:	
CC	Robert.Strausberg@nih.gov Tissue Procurement: Lee Helman, M.D.,	
CC	Michael R. Emmert-Buck, M.D., Ph.D. cDNA Library Preparation: David	
CC	B. Kitzman, Ph.D. cDNA Library Arrayed by: Greg Lennon, Ph.D. DNA	
CC	Sequencing by: Washington University Genome Sequencing Center Clon	
CC	distribution: NCI-CGAP clone distribution information can be found	
CC	through the I.M.A.G.E. Consortium/ILNI, at:	
CC	www-bio.lnl.gov/bcbp/image/image.html Insert Length: 379 Std	
CC	Error: 1000 Seq primer: 41m13 fwd. ET from Amersham.	
Key	Location/Qualifiers	

	source
FT	1..284
FT	/organism="Homo sapiens"
FT	/note="Vector: pAMP10; mRNA made from alveolar
FT	rhaddomyosarcoma, cDNA made by oligo-dT priming.
FT	Non-directionally cloned. Size-selected on agarose gel,
FT	average insert size 600 bp. Reference: Krizman et al.
FT	(1996) Cancer Research 56:3380-3383."
FT	/clone="923094"
FT	/clone_1lb="NCI_CGAP_Alvi1"
FT	/tissue_type="alveolar rhaddomyosarcoma"
FT	/lab_host="DH10B"
FT	<1..>284
FT	mRNA
FT	Sequence 284 BP; 97 A; 71 C; 72 G; 44 T; 0 other;
FT	90

	Query Match	7.8%	Score 11;	DB 65;	Length 284;
	Best Local Similarity	70.3%;	Pred. No. 5,	84e-62;	
	Matches 188;	Conservative	0;	Mismatches 47;	Indels 5; Gaps 4
Dd	37	tgaaccaggaatctcgacacgacctgggcagcatgycagaatccactctacaanaa	96		
Cp	1294	TGAACCTGAGATTGACACCAGCCTGTACACAATGGCGAATTCGCATTTTACCANAACA	1255		
Dd	97	gaccaaaaaaaaaaattagtctggcagtcgtgacacacacctgtgatccagtaactong	156		

Cp 1234 -A AAAACAAAAAGTTAATCAGGTGGTGGGCCCTTCCTTCCTGTAGTTCAGACTACT -AG 1179
 Db 157 gagcgcaagctgtgagagatctacttgaa -cagagaggttcagagctgcagatgacgtgcat 215
 Cp 1178 GAGACTAGGACGAGAGATACCTTTGAGCTCCAGAGGTAAAGCTCTCAGAGAGCATGCT 1119
 Db 216 tgcacacatcactccaagccttgataacagagcaagccgtatctccaataaaaaa 275
 Cp 1118 GGTCCTCACTGCATCCACGCTTGGTGTACAGAGTGAACCTCTTCAAAAA 1059

RESULT	11
ID	HS1275688
	standard; RNA; EST; 323 BP.

DT 24-JUN-1997 (Rel. 52, Created)
DT 28-JUN-1997 (Rel. 52, last updated, Version 2)
DE ne08902.s1 NCI-CGAP_Kid1 Homo sapiens CDNA clone 911378 similar to
DE contains Alu repetitive element;contains element Ll repetitive
DE element ;..

0S Homo sapiens (human)
0C Eukaryotea; mitochondrial eukaryotes; Metazoa; Chordata;
0C Vertebrata; Mammalia; Eutheria; Primates; Catarrhini; Hominoidea;
0C Homo.

RN [1]
RP 1-3

RA NCI-CGAP;
RT "National Cancer Institute, Cancer Genome Anatomy Project (CGAP)

```

RT      Tumor Gene Index";
RT      Unpublished.

```

CC Contact: Robert Strausberg, Ph.D. Tel: (301) 496-1550 Email:
CC Robert_Strausberg@nih.gov Tissue Procurement: L. Jeffrey Medeiros,
CC

CC M.D., Michael R. Emmert-Buck, M.D., Ph.D. cDNA Library Preparation
CC David B. Kitzman, Ph.D. cDNA Library Arrayed by: Greg Lennon, Ph.D

CC DNA Sequencing by: Washington University Genome Sequencing Center
CC Clone distribution: NCI-CGAP clone distribution information can be

CC found through the I.M.A.G.E. Consortium/LLNL at:
CC www.bio.llnl.gov/bbrp/image/image.html Insert here
CC

CC	Error: 0.00	Seq primer: -41ml3 fwd.	ET from Amersham
FH	Key	location/Qualifiers	

Source	FH	FT
--------	----	----

ET :
ET :
ET :

ET 1

ET E

ET

FT FT

ET
ET
mRNA

50 Sequence 323 BP; 63 A; 87 C; 72 G; 101 T; 0 other,

Query Match	7.7%;	Score 109;	DB 66;	Length 323;
Best Local Similarity	76.7%;	Pred. No. 2.42e-60;		

Matches 178; Conservative 0; Mismatches 51; Indels 3; Gaps 3

Db 38 accttttttttctgtgagagagctctgtctctgtcacccagctgcagtcagtggtg 97

QY 1057 ACTTTT TTTT TTTT TGACAGGCTC ACTCTGTGTCACCCAGGCTGGAGTGCAGTGGCA 1116

Db 98 cgatcttgcccaatgcacacctctgctgccaag-gttcaagaattctcttgccctcagcc 156

QY 1117 CCACATGGCTCTCTGCAGCCCTTACCTCTGGGAGCTCAAGTATCCTCTTGCCTCAGTC 1176

Db 157 tcccgagtagctgggactgcagggcatgcaccacacacacctgctaatTTTTTTgtatt 216

QY 1177 TCCT-AGTAGCTGCACTACAAGGAAGGGCCACACACCTGACTAATTGTTT 1235

Db 217 -tttagtgagacaggtttcaccatgtgccaagctagtctcaactcct 267

||||| 1236 GTTTGTAAGATGCATTTGCCATGTTGTACAGGCTGCTCAAACTCCT 1287

RESULT 12
LOCUS AA484267 323 bp mRNA EST 26-JUN-1997
DEFINITION ne88902.s1 NCI_CGAP_Kid1 Homo sapiens cDNA clone 911378 similar to
contains Alu repetitive element; contains element L1 repetitive
element ;.
ACCESSION AA484267
NID 92213080
KEYWORDS EST.
SOURCE human.
ORGANISM Homo sapiens
Eukaryotes; mitochondrial eukaryotes; Metazoa; Chordata;
Vertebrata; Mammalia; Eutheria; Primates; Catarrhini; Homnidae;
Homo.
REFERENCE 1 (bases 1 to 323)
AUTHORS NCI-CGAP.
TITLE National Cancer Institute, Cancer Genome Anatomy Project (CGAP),
Tumor Gene Index
JOURNAL Unpublished (1997)
COMMENT
Contact: Robert Strausberg, Ph.D.
Tel: (301) 496-1550
Email: Robert.Strausberg@nih.gov
Tissue Procurement: L. Jeffrey Medeiros, M.D., Michael R.
Emmert-Buck, M.D., Ph.D.
CDNA Library Preparation: David B. Krizman, Ph.D.
CDNA Library Arrayed by: Greg Lennon, Ph.D.
DNA Sequencing by: Washington University Genome Sequencing Center
Clone distribution: NCI-CGAP clone distribution information can be
found through the I.M.A.G.E. Consortium/LNL at:
www.bio.lnl.gov/bdrrp/image/image.html

Insert Length: 258 Std Error: 0.00
Seq primer: -41ml3 fwd. RT from Amersham.
Location/Qualifiers
1..323
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tumor, cDNA made by oligo-dT priming. Non-directionally
cloned. Size-selected on agarose gel, average insert
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Research 56:5380-5383."
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BASE COUNT mRNA
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ORIGIN

Query Match 7.7%; Score 109; DB 32; Length 323;
Best Local Similarity 76.7%; Pred. No. 2,42e-60;
Matches 178; Conservative 0; Mismatches 51; Indels 3; Gaps 3;

Db 38 acatttttttttttttgagagagctctgtcctgcacccaggctgagtcagtcagt 97
|||||
QY 1057 ACTTTTCTTTTCTTTTGTGACAGGCTGCACTGTGTCACCCAGGCTGAGTGCAGTGC 1116
|||||

Db 98 cgatctggcccaatgcacactctgcctgcag-gttcaagaattctctgtcctcagc 156
|||||
QY 1117 CCACCAAGGCTCTGAGCCTTGACCTCTGGAGCTCAAGTGAATCCTCCGCTCAATC 1176
|||||

Db 157 tcccgagtagctgagctgcagcagcagcagcagcagcagcagcagcagcagcagc 216
|||||
QY 1177 TCCT-AGTAGCTGGAACCTACAGAGAGAGGCCACACACCTACTACTTCTTTGTTT 1235
|||||

Db 217 -tttagtgagacagaggttcaccatgcttgccagagctagctcaaacctc 267
|||||
QY 1236 GTTTGTAAGATGCATTTGCCATGTTGTACAGGCTGCTCAAACTCCT 1287

||||| 13 AA502565 260 bp mRNA EST 10-JUL-1997
LOCUS ng62fi0.s1 NCI_CGAP_Lip2 Homo sapiens cDNA clone 939403 similar to
DEFINITION contains Alu repetitive element;.
ACCESSION AA502565
NID 92237532
KEYWORDS EST.
SOURCE human.
ORGANISM Homo sapiens
Eukaryotes; mitochondrial eukaryotes; Metazoa; Chordata;
Vertebrata; Mammalia; Eutheria; Primates; Catarrhini; Homnidae;
Homo.
REFERENCE 1 (bases 1 to 260)
AUTHORS NCI-CGAP.
TITLE National Cancer Institute, Cancer Genome Anatomy Project (CGAP),
Tumor Gene Index
JOURNAL Unpublished (1997)
COMMENT
Contact: Robert Strausberg, Ph.D.
Tel: (301) 496-1550
Email: Robert.Strausberg@nih.gov
Tissue Procurement: L. Jeffrey Medeiros, M.D., Michael R.
Emmert-Buck, M.D., Ph.D.
CDNA Library Preparation: David B. Krizman, Ph.D.
CDNA Library Arrayed by: Greg Lennon, Ph.D.
DNA Sequencing by: Washington University Genome Sequencing Center
Clone distribution: NCI-CGAP clone distribution information can be
found through the I.M.A.G.E. Consortium/LNL at:
www.bio.lnl.gov/bdrrp/image/image.html

Insert Length: 561 Std Error: 0.00
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High quality sequence stop: 133.
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/note="Vector: PAMPI0; mRNA made from liposarcoma. cDNA
made by oligo-dT priming. Non-directionally cloned.
Size-selected on agarose gel, average insert size 600 bp.
Reference: Krizman et al. (1996) Cancer Research
56:5380-5383."
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ORIGIN

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Matches 178; Conservative 0; Mismatches 40; Indels 5; Gaps 5;

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|||||

Db 61 gtcatgctcactgcagcctcaacctccag-ggccaaagtatctccagcctcagctc 119
|||||
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|||||

Db 120 ctgagtagctgagacttacacacacacacagcagcctgctaattttgtatctttt 179
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QY 1179 CT-AGTAGCTGGAACCT-ACAAGAGAGGCCACACACACTGACTGACTTCTTTGTTT 1236
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Db 180 ttg-tagagatggggtttcaacatgtttgccagagctgtctc 221
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RESULT 14
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NI 92237532
DT 04-JUL-1997 (Rel. 52, Created)
DT 12-JUL-1997 (Rel. 52, Last updated, Version 2)
DE n962f10.s1 NCI-CGAP_L1p2 Homo sapiens cDNA clone 939403 similar to
DE contains Alu repetitive element;.
KW ESR.
OS Homo sapiens (human)
OC Eukaryota; Eukaryota; Chordata;
OC Vertebrata; Mammalia; Eutheria; Primates; Catarrhini; Homnidae;
OC Homo.
RN [1]
RP 1-360
RA NCI-CGAP;
RT "National Cancer Institute, Cancer Genome Anatomy Project (CGAP),
RT Tumor Gene Index";
RT Unpublished.
CC Contact: Robert Strausberg, Ph.D. Tel: (301) 496-1550 Email:
CC Robert.Strausberg@nih.gov Tissue Procurement: L. Jeffrey Medeiros,
CC M.D., Michael R. Emmert-Buck, M.D., Ph.D. cDNA Library Preparation:
CC David B. Krizman, Ph.D. cDNA Library Arrayed by: Greg Lennon, Ph.D.
CC DNA Sequencing by: Washington University Genome Sequencing Center
CC Clone distribution: NCI-CGAP clone distribution information can be
CC found through the I.M.A.G.E. Consortium/LINC at:
CC www.bio.lnlni.gov/dbrrp/image/image.html Insert Length: 561 Std
CC Error: 0.00 Seq primer: -40m13 fwd. ET from Amersham High quality
CC sequence stop: 133.
FH Key Location/Qualifiers
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FT /note="Vector: pMP10; mRNA made from l1posarcoma, cDNA
FT made by oligo-dt priming. Non-directionally cloned.
FT Size-selected on agarose gel, average insert size 600 bp.
FT Reference: Krizman et al. (1996) Cancer Research
FT 56:5380-5383."
FT /clone="939403"
FT /clone_l1b="NCI-CGAP_L1p2"
FT /tissue_type="l1posarcoma"
FT /lab_host="DH10B"
FT mRNA
FT sequence 260 BP: 47 A; 73 C; 60 G; 80 T; 0 other;
SQ
Query Match 7.6%; Score 108; DB 69; Length 260;
Best Local Similarity 79.8%; Pred. No. 1.56e-59;
Matches 178; Conservative 0; Mismatches 40; Indels 5; Gaps 5;
D 2 ttttttttttttgagcagaggtcttcgccctgctc-cccagagctgagtgagtgatg 60
D ||||||| ||||||| ||||||| ||||||| ||||||| ||||||| |||||||
D 1059 ttttttttttttttttttttttggacagggtctactctgtcaccacaggctgagtgacg 1118
D ||||||| ||||||| ||||||| ||||||| ||||||| ||||||| |||||||
D 61 gtcatagtcactgcagagctcaactccacag-gcccaagtgaactccagagctcagctc 119
D ||||||| ||||||| ||||||| ||||||| ||||||| ||||||| |||||||
D 1119 acgatgctctctgcagccttgacctctgggagctcactgaagtatctcttcgctcagctc 1178
D ||||||| ||||||| ||||||| ||||||| ||||||| ||||||| |||||||
D 120 ctgagtagctgaggaactcaacaacacacacagcagcagcctgagctaaattttgtattttt 179
D ||||||| ||||||| ||||||| ||||||| ||||||| ||||||| |||||||
D 1179 ct-AGTACTGGAAGT-ACAAGGAAGGAGCCACACACCGTACTACTTTTGTGTTTGG 1236
D ||||||| ||||||| ||||||| ||||||| ||||||| ||||||| |||||||
D 180 ttgt-tagagatggggtttcacacatggttgcacagagctgtctc 221
D ||||||| ||||||| ||||||| ||||||| ||||||| ||||||| |||||||
D 1237 ttttgctaaagatggcatttgcgcagtggttgcacagagctgcttc 1279
D ||||||| ||||||| ||||||| ||||||| ||||||| ||||||| |||||||

RESULT 15
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DEFINITION z517c02.t1 NCI-CGAP_GCB1 Homo sapiens cDNA clone 683442.5 similar
to contains Alu repetitive element;contains element MSRI repetitive
element;.
ACCESSION AA262532
NID 91897894
KEYWORDS ESR.
SOURCE human

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ORGANISM	Homo sapiens Eukaryote; mitochondrial eukaryotes; Metazoa; Chordata; Vertebrata; Mammalia; Eutheria; Primates; Catarrhini; Hominiidae; Homo. 1 (bases 1 to 300)
REFERENCE AUTHORS	NCI-CCAP. National Cancer Institute, Cancer Genome Anatomy Project (CGAP), Tumor Gene Index Unpublished (1997)
JOURNAL	
COMMENT	Contact: Robert Strausberg, Ph.D. Tel: (301) 496-1550 Email: Robert_Strausberg@nih.gov This clone is available royalty-free through LIND ; contact the IMAGE Consortium (info@image.lnl.gov) for further information. Putative full length read The vector to vector length is Seq primer: -28ml3 rev2 Err from Amersham.
FEATURES	Location/Qualifiers
SOURCE	1..300
	/organism="Homo sapiens" /note="Vector: pPT13D-Pac (Pharmacia) with a modified polylinker; Site_1: Not I; Site_2: Eco RI; 1st strand cDNA was prepared from human tonsillar cells enriched for germinal center B cells by flow sorting (CD20+, IgD-), provided by Dr. Louis W. Staudt (NCI). CDNA synthesis was primed with a Not I - Oligo(dT) primer [5'-GTTCACCAATCTGAAGTGAGGAGCGGCCGCCTCATTTTTTTTTTTT- 3']. Double-stranded cDNA was ligated to Eco RI adaptors (pharmacia), digested with Not I and cloned into the Not I and Eco RI sites of the modified pT713 vector. Library went through one round of normalization, and was constructed by Bento Soares and M. Fatima Bonaldo."
	/clone_1lb="NCI CGAP GCBI" /clone_1lb="685442" /tissue_type="germinal center B cell" /lab_host="DH10B"
BASE COUNT	mRNA 86 a 71 c 77 g 66 t <1...>300
ORIGIN	
Query Match	7.6%; Score 108; DB 20; Length 300;
Best Local Similarity	76.2%; Pred. No.1.56e-59;
Matches 179; Conservative	0; Mismatches 53; Indels 3; Gaps 3;
Db	68 ttggaggagactcttgagcccgcaaatltagaacaccactgaggcagaatagtgaacctta 127
Cp	1307 TGGGAGGGCCAAGGAACTTAGAATTGTAACACCAGCCTGTACAACATGAGGGAATGCGCA 1248
Db	128 tctctattaaa-aaaaattaataaaattagccaggcgatgagggcacacactgtaattcc 186
Cp	1247 TCTTTACCAAAACAAAAAACAAAAGAATGACGATGTGTGGCCCTTCTTGTAAGTTC 1188
Db	187 agctactcagaagagcttagagcaagaagttaacttagagc-ccaagagatcgagagctgtatc 245
Cp	1187 AGCTACTT-AGGAGACTGAGGCGAGGAGTACTCTTGAGCTCCACAGAGGTCAAAGCGTCGCA 1129
Db	246 gagctatgattgggccactgtcaccttagacctgtggcgatagatatagagacctgtgca 300
Cp	1128 GAGCGATGTGTGTGCACATGCACATCCAGCCCTGGGGTGAACAGATGAGACCCGTCTCA 1074

Search completed: Wed Mar 25 14:03:35 1998
Job time : 532 secs.

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MIRAGE

(TM)

Release 2.1D John F. Collins, Biocomputing Research Unit.
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Msrch_n n.a. - n.a. database search, using Smith-Waterman algorithm
on: Wed Mar 25 14:03:54 1998; MasPar time 76.15 Seconds
854.742 Million cell updates/sec
Similar output not generated.

Title: >US-08-236-918A-7
(1-1415) from 5674704.seq
Description: 1415
Perfect Score: 1415
N.A. Sequence: 1 AGTGGAAAGTCTCCGCGAG.....TGATTAATAAAAAAAAAA 1415
Comp: TCACCTTCAAGAGCGCGTC.....ACTATTTTTTTTTTTTTT

Scoring table: TABLE default
Gap 6

Nmatch STD : Dbase 0; Query 0

Searched: 87538 seqs, 2299015 bases x 2

Post-processing: Minimum Match 0%

Listing first 45 summaries

Database:

n-issued
1:back1 2:51 3:52 4:53 5:54 6:55 7:56 8:57 9:PCPT90
10:PCPT91 11:PCPT92 12:PCPT93 13:PCPT94 14:PCPT95 15:PCPT96

Statistics: Mean 9.033; Variance 5.543; scale 1.630

Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description	Pred. No.
1	1415	100.0	1415	7	US-08-236-Sequence 7, Applicatio	0.00e+00
2	836	59.1	838	13	PCPT-US94-1 Sequence 1, Applicati	0.00e+00
3	836	59.1	838	15	PCPT-US96-0 Sequence 7, Applicatio	0.00e+00
4	233	16.5	2347	15	PCPT-US96-0 Sequence 1, Applicatio	1.35e-135
5	229	16.2	768	7	US-08-236-Sequence 5, Applicatio	7.20e-133
6	105	7.4	6769	14	PCPT-US95-1 Sequence 20, Applicati	9.80e-50
7	105	7.4	6769	14	PCPT-US95-1 Sequence 20, Applicati	9.80e-50
8	105	7.4	6769	14	PCPT-US95-1 Sequence 20, Applicati	9.80e-50
9	105	7.4	6769	14	PCPT-US95-1 Sequence 20, Applicati	9.80e-50
10	103	7.3	2048	5	US-08-480-Sequence 11, Applicati	1.96e-48
11	103	7.3	2048	4	US-07-602-Sequence 11, Applicati	1.96e-48
12	101	7.1	7210	14	PCPT-US95-0 Sequence 10, Applicati	3.91e-47
13	101	7.1	22481	14	PCPT-US95-0 Sequence 43, Applicati	3.91e-47
14	99	7.0	20303	7	US-08-370-Sequence 6, Applicatio	7.75e-46
15	99	7.0	26764	7	US-08-370-Sequence 1, Applicatio	7.75e-46
16	97	6.9	2362	6	US-08-265-Sequence 3, Applicatio	1.53e-44
17	98	6.9	5095	5	US-08-092-Sequence 3, Applicatio	3.44e-45
18	98	6.9	19011	7	US-08-310-Sequence 36, Applicati	3.44e-45
19	98	6.9	19557	11	PCPT-US92-0 Sequence 1, Applicatio	3.44e-45

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c	21	96	6.8	31571	7	US-08-323	Sequence 1, Applicatio	6.77e-44
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c	23	95	6.7	22481	14	PCT-US95-0	Sequence 43, Applicati	2.99e-43
c	24	94	6.6	1323	15	PCT-US96-1	Sequence 15, Applicati	1.32e-42
c	25	93	6.6	1804	12	PCT-US93-0	Sequence 82, Applicati	5.83e-42
c	26	94	6.6	2619	15	PCT-US96-1	Sequence 17, Applicati	1.32e-42
c	27	94	6.6	2887	15	PCT-US96-1	Sequence 14, Applicati	1.32e-42
c	28	94	6.6	4421	14	PCT-US95-0	Sequence 9, Applicatio	2.57e-41
c	29	92	6.5	1545	7	US-08-446	Sequence 6, Applicatio	2.57e-41
c	30	92	6.5	1545	7	US-08-446	Sequence 4, Applicatio	2.57e-41
c	31	92	6.5	5836	7	US-08-380	Sequence 1, Applicatio	2.57e-41
c	32	92	6.5	17327	4	US-07-906	Sequence 15, Applicati	4.96e-40
c	33	92	6.5	1301	15	PCT-US96-1	Sequence 19, Applicati	4.96e-40
c	34	90	6.4	1363	14	PCT-US95-0	Sequence 21, Applicati	4.96e-40
c	35	90	6.4	1443	15	PCT-US96-1	Sequence 33, Applicati	4.96e-40
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c	37	91	6.4	3590	15	PCT-US96-0	Sequence 1, Applicatio	1.13e-40
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c	44	91	6.4	17327	4	US-07-906	Sequence 15, Applicati	1.13e-40
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ALIGNMENTS

RESULT 1
ID US-08-236-918A-7 STANDARD; DNA; UNC; 1415 BP.
AC xxxxxx
DT 01-JAN-1900
DE Sequence 7, Application US/08236918A.
CC Sequence 7, Application US/08236918A
CC Patent No. 5674704
CC GENERAL INFORMATION:
CC APPLICANT: Alderson, Mark R.
CC APPLICANT: Goodwin, Raymond G.
CC APPLICANT: Smith, Craig A.
CC TITLE OF INVENTION: Cytokine Designated 4-1BB Ligand
CC NUMBER OF SEQUENCES: 18
CC CORRESPONDENCE ADDRESS:
CC ADDRESSEE: Kathryn A. Anderson, Immunex Corporation
CC STREET: 51 University Street
CC CITY: Seattle
CC STATE: Washington
CC COUNTRY: US
CC ZIP: 98101
CC COMPUTER READABLE FORM:
CC MEDIUM TYPE: Floppy disk
CC COMPUTER: Apple Power Macintosh
CC OPERATING SYSTEM: Apple 7.5.3
CC SOFTWARE: Microsoft Word, Version #6.0.1
CC CURRENT APPLICATION DATA:
CC APPLICATION NUMBER: US/08/236, 918A
CC FILING DATE: 06-May-1994
CC CLASSIFICATION: 435
CC PRIOR APPLICATION DATA:
CC APPLICATION NUMBER: US 08/060, 843
CC FILING DATE: 07-May-1993
CC CLASSIFICATION: 435
CC ATTORNEY/AGENT INFORMATION:
CC NAME: Anderson, Kathryn A.
CC REGISTRATION NUMBER: 32,172
CC REFERENCE/DOCKET NUMBER: 2801-B
CC TELECOMMUNICATION INFORMATION:
CC TELEPHONE: (206) 587-0430
CC TELEFAX: (206) 233-0644
CC INFORMATION FOR SEQ ID NO: 7:
CC SEQUENCE CHARACTERISTICS:
CC LENGTH: 1415 base pairs

CC TYPE: nucleic acid
 CC STRANDEDNESS: single
 CC TOPOLOGY: linear
 CC MOLECULE TYPE: cDNA to mRNA
 CC HYPOTHETICAL: NO
 CC ANTI-SENSE: NO
 CC IMMEDIATE SOURCE:
 CC CLONE: hu4-1BB
 CC FEATURE:
 CC NAME/KEY: CDS
 CC LOCATION: 120..887
 CC FEATURE:
 CC NAME/KEY: mat-peptide
 CC LOCATION: 189..884
 CC FEATURE:
 CC NAME/KEY: sig-peptide
 CC LOCATION: 120..188
 CC Sequence 1415 BP; 385 A; 332 C; 333 G; 365 T; 0 other;

Query Match 100.0%; Score 1415; DB 7; Length 1415;

Local Similarity 100.0%; Pred.No. 0.00e+00; Mismatches 0; Indels 0; Gaps 0;

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QY 721 TCCGTGCTGTTCTCTCAAGCTCGCTTCTCTGTTTAAAGGGGAGGAGAAAGTCC 780
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 QY 781 TGTATATATCAACCAACCATTTTGTGAGCAGTACAACTACTCAAGAGAGATGGCT 840
 DB 841 GTAGCTGCCATTTCCAGAGAGAGAGAGAGAGATGTGAATCTGAAATGGAATCAAT 900
 QY 841 GTAGCTGCCATTTCCAGAGAGAGAGAGAGAGATGTGAATCTGAAATGGAATCAAT 900
 DB 901 AGGCGTGTGGAGCTTCTTGAAGAGAGAGAGAGAGATATGATCATCCGCTATCAGAGC 960
 QY 901 AGGCGTGTGGAGCTTCTTGAAGAGAGAGAGAGAGATATGATCATCCGCTATCAGAGC 960
 DB 961 TTTCAAAAAGCAAGAACACCATCTCAATATACCAGAGATTTCCCAACACAGCTTCTT 1020
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RESULT 2
 ID PCT-US94-10457-1 STANDARD; DNA; UNC; 838 BP.
 AC xxxxxx
 DT 01-JAN-1900
 DE Sequence 1, Application PC/TUS9410457.
 CC Sequence 1, Application PC/TUS9410457
 CC GENERAL INFORMATION:
 CC APPLICANT: Byoung Se Kwon
 CC TITLE OF INVENTION: New Human Receptor and Related Products
 CC NUMBER OF SEQUENCES: 1
 CC ADDRESSEE: Barnard & Brown
 CC STREET: 306 E. State St., Suite 220
 CC CITY: Ithaca
 CC STATE: New York
 CC COUNTRY: United States
 CC ZIP: 14850
 CC COMPUTER READABLE FORM:
 CC MEDIUM TYPE: Diskette, 3.50 inch, 1.4mb storage
 CC COMPUTER: IBM AT Compatible
 CC OPERATING SYSTEM: MS DOS, Version 5.0
 CC SOFTWARE: Special Qbasic program
 CC CURRENT APPLICATION DATA:
 CC APPLICATION NUMBER: PCT/US94/10457
 CC FILING DATE:

CC CLASSIFICATION:
 CC PRIOR APPLICATION DATA:
 CC APPLICATION NUMBER: 08/012,269
 CC FILING DATE: 2/1/93
 CC PRIOR APPLICATION DATA:
 CC APPLICATION NUMBER: 07/922,996
 CC FILING DATE: 7/30/92
 CC PRIOR APPLICATION DATA:
 CC APPLICATION NUMBER: 07/267,577
 CC FILING DATE: 11/7/98
 CC ATTORNEY/AGENT INFORMATION:
 CC NAME: Michaels, Christopher A.
 CC REGISTRATION NUMBER: 34,390
 CC REFERENCE/DOCKET NUMBER: kmh41db
 CC TELECOMMUNICATION INFORMATION:
 CC TELEPHONE: 607-273-1711
 CC TELEFAX: 607-273-2609
 CC TELEX:
 CC INFORMATION FOR SEQ ID NO: 1:
 CC SEQUENCE CHARACTERISTICS:
 CC LENGTH: 838
 CC TYPE: nucleic acid
 CC STRANDEDNESS: double stranded
 CC TOPOLOGY: linear
 CC MOLECULE TYPE: linear
 CC HYPOTHETICAL: NO
 CC ANTI-SENSE: NO
 CC FRAGMENT TYPE: n/a
 CC ORIGINAL SOURCE:
 CC ORGANISM: Human
 CC STRAIN:
 CC INDIVIDUAL ISOLATE: H4-1BB #1
 CC DEVELOPMENTAL STAGE: Differentiated T-cell
 CC HAPLOTYPE:
 CC TISSUE TYPE:
 CC CELL TYPE: Lymphocytes
 CC CELL LINE:
 CC ORGANELLER:
 CC IMMEDIATE SOURCE:
 CC LIBRARY: cDNA library
 CC CLONE:
 CC POSITION IN GENOME:
 CC CHROMOSOME/SEGMENT:
 CC MAP POSITION:
 CC UNITS:
 CC FEATURE:
 CC NAME/KEY: H4-1BB
 CC LOCATION:
 CC IDENTIFICATION METHOD: Similarity to mouse 4-1BB and other
 CC IDENTIFICATION METHOD: members of NGFR superfamily
 CC OTHER INFORMATION:
 CC PUBLICATION INFORMATION:
 CC AUTHORS: Kwon, B.S., and Weissman, S.M.
 CC TITLE: cDNA sequences of two inducible T-cell genes
 CC JOURNAL: Proc. Natl. Acad. Sci. USA
 CC VOLUME: 86
 CC ISSUE:
 CC PAGES: 1963-1967
 CC RELEVANT RESIDUES IN SEQ ID NO: all
 CC Sequence 838 BP: 218 A; 191 C; 215 G; 214 T; 0 other:
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 CC Query Match 59.1%; Score 836; DB 13; Length 838;
 CC Best Local Similarity 99.9%; Pred. No. 0.00e+00;
 CC Matches 837; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

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 AC xxxxxx
 DE 01-JAN-1900
 DE Sequence 7, Application PC/TUS9603965.
 CC Sequence 7, Application PC/TUS9603965
 CC GENERAL INFORMATION:
 CC APPLICANT: Kwon, Byoung Se
 CC TITLE OF INVENTION: Monoclonal antibody against human
 CC TITLE OF INVENTION: receptor 4-1BB
 CC NUMBER OF SEQUENCES: 10
 CC CORRESPONDENCE ADDRESS:
 CC ADDRESSEE: Barnard, Brown & Michaels
 CC STREET: 306 East State Street, Suite 220
 CC CITY: Ithaca
 CC STATE: NY
 CC COUNTRY: USA
 CC ZIP: 14850
 CC COMPUTER READABLE FORM:
 CC MEDIUM TYPE: Floppy disk
 CC COMPUTER: IBM PC compatible
 CC OPERATING SYSTEM: PC-DOS/MS-DOS
 CC SOFTWARE: PatentIn Release #1.0, Version #1.30

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CC CURRENT APPLICATION DATA:
CC APPLICATION NUMBER: PCT/US96/03965
CC FILING DATE:
CC CLASSIFICATION:
CC PRIOR APPLICATION DATA:
CC APPLICATION NUMBER: US 08/122,796
CC FILING DATE: 16-SEP-1993
CC PRIOR APPLICATION DATA:
CC APPLICATION NUMBER: US 08/012,269
CC FILING DATE: 01-FEB-1993
CC PRIOR APPLICATION DATA:
CC APPLICATION NUMBER: US 07/922,996
CC FILING DATE: 30-JUL-1992
CC PRIOR APPLICATION DATA:
CC APPLICATION NUMBER: US 07/267,577
CC FILING DATE: 07-NOV-1988
CC ATTORNEY/AGENT INFORMATION:
CC NAME: Michaels, Christopher A
CC REGISTRATION NUMBER: 34,390
CC REFERENCE/DOCKET NUMBER: KROS
CC TELECOMMUNICATION INFORMATION:
CC TELEPHONE: 607-273-1711
CC TELEFAX: 607-273-2609
CC INFORMATION FOR SEQ ID NO: 7:
CC SEQUENCE CHARACTERISTICS:
CC LENGTH: 838 base pairs
CC TYPE: nucleic acid
CC STRANDEDNESS: double
CC TOPOLOGY: linear
CC MOLECULE TYPE: cDNA to mRNA
CC HYPOTHETICAL: NO
CC ANTI-SENSE: NO
CC ORIGINAL SOURCE:
CC ORGANISM: Homo sapiens
CC INDIVIDUAL ISOLATE: H4-1BB #1
CC DEVELOPMENTAL STAGE: Differentiated T-cell
CC CELL TYPE: Lymphocyte
CC FEATURE:
CC NAME/KEY: CDS
CC LOCATION: 41..805
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CC OTHER INFORMATION: /product= "H4-1BB"
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CC LOCATION: 41..802
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CC OTHER INFORMATION: /product= "H4-1BB"
CC OTHER INFORMATION: /number= 1
CC Sequence 838 bp; 218 A; 191 C; 215 G; 214 T; 0 other;
CC Query Match 59.1%; Score 836; DB 15; Length 838;
CC Best Local Similarity 99.9%; Pred. No. 0.00e+00;
CC Matches 837; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
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Cc |||||||
Cc |||||||
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Cc |||||||
Cc Db 121 TTGAGTAGAACGCCAGCGTGGTACTATCTCGATTAATAAGAGAATGAGATTTCAGATCC 180
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Cc |||||||
Cc |||||||
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Cc |||||||
Cc |||||||
Cc Qy 260 CTGTCTCCAATAGATTCTCCACGCGAGGTGGCAAAGACCTGTGACATATGCAAGCA 319
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Db	481	TGTGATGGGACGAGAGGAGGAGCGTGTGTCTGTGACCATCTTCACGTACCTCTCTCC	540
QY	560	TGTGATGGGACGAGAGGAGGAGCGTGTGTCTGTGACCATCTTCACCGACCTCTCTCC	619
Db	541	GGGAGCATCCCTGTGTGACCCCGCTGGCCCTGCGAGAGAGCCAGACACTCTCCGAGAT	600
QY	620	GGGAGCATCCCTGTGTGACCCCGCTGGCCCTGCGAGAGAGCCAGACACTCTCCGAGAT	679
Db	601	CATCCTCTTCTTTCTTGGCGTGAAGCTGACGTCGTCCTCTCTCTCTCTCTCTCTCTCCAC	660
QY	680	CATCCTCTTCTTTCTTGGCGTGAAGCTGACGTCGTCCTCTCTCTCTCTCTCTCTCTCCAC	739
Db	661	GCTCGTTTCTCTGTGTGTTAAACGGGGCGACGAAAGAACTCTGTATATATTCAAACACC	720
QY	740	GCTCGTTTCTCTGTGTGTTAAACGGGGCGACGAAAGAACTCTGTATATATTCAAACACC	799
Db	721	ATTATGAGACCACTACAACTACTCAAGAGGAAGATGCGTGTAGCTGCCGATTTCAGA	780
QY	800	ATTATGAGACCACTACAACTACTCAAGAGGAAGATGCGTGTAGCTGCCGATTTCAGA	859
Db	781	AGAAGAAAGAGGAGATGTGAACGTGAATAATGGAAGTCAATAGGCGCTGTGGGACTTT	838
QY	860	AGAAGAAAGAGGAGATGTGAACGTGTGAATAATGGAAGTCAATAGGCGCTGTGGGACTTT	917
RESULT	4	PCT-US96-03965-1 STANDARD; DNA; UNC; 2347 BP.	
ID	AC	xxxxxx	
DT	01-JAN-1900		
DE	Sequence 1, Application PC/TUS9603965.		
CC	Sequence 1, Application PC/TUS9603965		
CC	GENERAL INFORMATION:		
CC	APPLICANT: Kwon, Byoung Se		
CC	TITLE OF INVENTION: Monoclonal antibody against human		
CC	TITLE OF INVENTION: receptor 4-1BB		
CC	NUMBER OF SEQUENCES: 10		
CC	CORRESPONDENCE ADDRESS:		
CC	ADDRESSEE: Barnard, Brown & Michaels		
CC	STREET: 306 East State Street, Suite 220		
CC	CITY: Ithaca		
CC	STATE: NY		
CC	COUNTRY: USA		
CC	ZIP: 14850		
CC	COMPUTER READABLE FORM:		
CC	MEDIUM TYPE: floppy disk		
CC	COMPUTER: IBM PC compatible		
CC	OPERATING SYSTEM: PC-DOS/MS-DOS		
CC	SOFTWARE: PatentIn Release #1.0, Version #1.30		
CC	CURRENT APPLICATION DATA:		
CC	APPLICATION NUMBER: PCT/US96/03965		
CC	FILING DATE:		
CC	CLASSIFICATION:		
CC	PRIOR APPLICATION DATA:		
CC	APPLICATION NUMBER: US 08/122,796		
CC	FILING DATE: 16-SEP-1993		
CC	PRIOR APPLICATION DATA:		
CC	APPLICATION NUMBER: US 08/012,269		
CC	FILING DATE: 01-FEB-1993		

CC 1286 GAGTTGAGACGACGCTGTACACATGCGGAATGCCATCTTACCAACAAAAACAA 1227
DB 2850 AAAAAATTAACCCGGGGTGGTGGCTATGCTGTATCCAGCTACTAGAGAGGCTGAGGC 2909
CC 1226 AAAAGTAGTGACGTGGTGGCCCTCTTGTAGTTCAGCTACT -AGGAGACTGAGGC 1168
DB 2910 AGGAGATCCCTTGAAC -CCAGAGAGCAGAGGTGACAGTGCAGCAAGATGCACCATTTGC 2968
CC 1167 AGGAGATCATTGAGTCCAGAGGTCAGAGCTGCAGAGAGCCATGCTGCCACTGC 1108
DB 2969 ACTCCAGCCTAGGACACAGAGTGAATCCATCTCAAAAAAAAAAAAAA 3018
CC 1107 ACTCCAGCCTGGTGACCA -GAGTGAGACCCCTGTCAAAAAAAAAAAAAA 1059

RESULT 7
ID PCT-US95-10203-20 STANDARD; DNA; UNC; 6769 BP.
AC xxxxxx
DT 01-JAN-1900
Sequence 20, Application PC/TUS9510203.
GENERAL INFORMATION:
CC APPLICANT: Skolnick, Mark H.
CC APPLICANT: Goldgar, David E.
CC APPLICANT: Miki, Yoshio
CC APPLICANT: Swenson, Jeff
CC APPLICANT: Kamb, Alexander
CC APPLICANT: Harshman, Keith D.
CC APPLICANT: Shattuck-Eidens, Donna M.
CC APPLICANT: Tavtigian, Sean V.
CC APPLICANT: Wiseman, Roger W.
CC APPLICANT: Futreal, P. Andrew
CC TITLE OF INVENTION: 17q-Linked Breast and Ovarian Cancer
CC TITLE OF INVENTION: Susceptibility Gene
CC NUMBER OF SEQUENCES: 85
CC CORRESPONDENCE ADDRESSES:
CC ADDRESSEE: Venable, Baetjer, Howard & Civiletti, LLP
CC STREET: 1201 New York Avenue, N.W., Suite 1000
CC CITY: Washington
CC STATE: DC
CC COUNTRY: USA
CC ZIP: 20005
CC COMPUTER READABLE FORM:
CC MEDIUM TYPE: Floppy disk
CC COMPUTER: IBM PC compatible
CC OPERATING SYSTEM: PC-DOS/MS-DOS
CC SOFTWARE: PatentIn Release #1.0, Version #1.30
CC CURRENT APPLICATION DATA:
CC APPLICATION NUMBER: PCT/US95/10203
CC FILING DATE:
CC CLASSIFICATION:
CC PRIOR APPLICATION DATA:
CC APPLICATION NUMBER: US
CC FILING DATE: 07-JUN-1995
CC PRIOR APPLICATION DATA:
CC APPLICATION NUMBER: US 08/409,305
CC FILING DATE: 24-MAR-1995
CC PRIOR APPLICATION DATA:
CC APPLICATION NUMBER: US 08/348,824
CC FILING DATE: 29-NOV-1994
CC PRIOR APPLICATION DATA:
CC APPLICATION NUMBER: US 08-308,104
CC FILING DATE: 16-SEP-1994
CC PRIOR APPLICATION DATA:
CC APPLICATION NUMBER: US 08/300,266
CC FILING DATE: 02-SEP-1994
CC PRIOR APPLICATION DATA:
CC APPLICATION NUMBER: US 08/289,221
CC FILING DATE: 12-AUG-1994
CC ATTORNEY/AGENT INFORMATION:
CC NAME: Ihnen, Jeffrey L.
CC REGISTRATION NUMBER: 28,957
CC REFERENCE/DOCKET NUMBER: 24884-109347

CC TELECOMMUNICATION INFORMATION:
CC TELEPHONE: 202-962-4810
CC TELEFAX: 202-962-8300
CC INFORMATION FOR SEQ ID NO: 20:
CC SEQUENCE CHARACTERISTICS:
CC LENGTH: 6769 base pairs
CC TYPE: nucleic acid
CC STRANDEDNESS: double
CC TOPOLOGY: linear
CC MOLECULE TYPE: DNA (genomic)
CC HYPOTHEICAL: NO
CC ANTI-SENSE: NO
CC ORIGINAL SOURCE:
CC ORGANISM: Homo sapiens
CC Sequence 6769 BP; 1954 A; 1377 C; 1469 G; 1937 T; 32 other;
SQ
Query Match 7.4%; Score 105; DB 14; Length 6769;
Best Local Similarity 76.1%; Pred. No. 9,80e-50;
Matches 175; Conservative 0; Mismatches 52; Indels 3; Gaps 3;
DB 2790 GAGTTGAGACGACGCTGTACACATGAGAGAAACCCCATCTCTACTAAAAA 2849
CC 1286 GAGTTGAGACGACGCTGTACACATGAGAGAAATGCACTTTACCAACAAAAACAA 1227
DB 2850 AAAAAATTAACCCGGGGTGGTGGCTATGCTGTATCCAGCTACTAGAGAGGCTGAGGC 2909
CC 1226 AAAAGTAGTGACGTGGTGGCCCTCTTGTAGTTCAGCTACT -AGGAGACTGAGGC 1168
DB 2910 AGGAGATCCCTTGAAC -CCAGAGAGCAGAGGTGACAGTGCAGCAAGATGCACCATTTGC 2968
CC 1167 AGGAGATCATTGAGTCCAGAGGTCAGAGCTGCAGAGAGCCATGCTGCCACTGC 1108
DB 2969 ACTCCAGCCTAGGACACAGAGTGAATCCATCTCAAAAAAAAAAAAAA 3018
CC 1107 ACTCCAGCCTGGTGACCA -GAGTGAGACCCCTGTCAAAAAAAAAAAAAA 1059

RESULT 8
ID PCT-US95-10220-20 STANDARD; DNA; UNC; 6769 BP.
AC xxxxxx
DT 01-JAN-1900
Sequence 20, Application PC/TUS9510220.
GENERAL INFORMATION:
CC APPLICANT: Skolnick, Mark H.
CC APPLICANT: Goldgar, David E.
CC APPLICANT: Miki, Yoshio
CC APPLICANT: Swenson, Jeff
CC APPLICANT: Kamb, Alexander
CC APPLICANT: Harshman, Keith D.
CC APPLICANT: Shattuck-Eidens, Donna M.
CC APPLICANT: Tavtigian, Sean V.
CC APPLICANT: Wiseman, Roger W.
CC APPLICANT: Futreal, P. Andrew
CC TITLE OF INVENTION: Method for Diagnosing a
CC TITLE OF INVENTION: Predisposition for Breast and Ovarian Cancer
CC NUMBER OF SEQUENCES: 85
CC CORRESPONDENCE ADDRESSES:
CC ADDRESSEE: Venable, Baetjer, Howard & Civiletti, LLP
CC STREET: 1201 New York Avenue, N.W., Suite 1000
CC CITY: Washington
CC STATE: DC
CC COUNTRY: USA
CC ZIP: 20005
CC COMPUTER READABLE FORM:
CC MEDIUM TYPE: Floppy disk
CC COMPUTER: IBM PC compatible
CC OPERATING SYSTEM: PC-DOS/MS-DOS
CC SOFTWARE: PatentIn Release #1.0, Version #1.30
CC CURRENT APPLICATION DATA:
CC APPLICATION NUMBER: PCT/US95/10220
CC FILING DATE:
CC CLASSIFICATION:

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CC      PRIOR APPLICATION DATA:
CC      APPLICATION NUMBER: US
CC      FILING DATE: 07-JUN-1995
CC      PRIOR APPLICATION DATA:
CC      APPLICATION NUMBER: US 08/409,305
CC      FILING DATE: 24-MAR-1995
CC      PRIOR APPLICATION DATA:
CC      APPLICATION NUMBER: US 08/348,824
CC      FILING DATE: 29-NOV-1994
CC      PRIOR APPLICATION DATA:
CC      APPLICATION NUMBER: US 08-308,104
CC      FILING DATE: 16-SEP-1994
CC      PRIOR APPLICATION DATA:
CC      APPLICATION NUMBER: US 08/300,266
CC      FILING DATE: 02-SEP-1994
CC      PRIOR APPLICATION DATA:
CC      APPLICATION NUMBER: US 08/289,221
CC      FILING DATE: 12-AUG-1994
CC      ATTORNEY/AGENT INFORMATION:
CC      NAME: Ihnen, Jeffrey L.
CC      REGISTRATION NUMBER: 28,957
CC      REFERENCE/DOCKET NUMBER: 24884-109347
CC      TELECOMMUNICATION INFORMATION:
CC      TELEPHONE: 202-962-4810
CC      TELEFAX: 202-962-8300
CC      INFORMATION FOR SEQ ID NO: 20:
CC      SEQUENCE CHARACTERISTICS:
CC      LENGTH: 6769 base pairs
CC      TYPE: nucleic acid
CC      STRANDEDNESS: double
CC      TOPOLOGY: linear
CC      MOLECULE TYPE: DNA (genomic)
CC      HYPOTHETICAL: NO
CC      ANTI-SENSE: NO
CC      ORIGINAL SOURCE:
CC      ORGANISM: Homo sapiens
SQ      Sequence 6769 bp: 1954 A; 1377 C; 1469 G; 1937 T; 32 other;

Query Match          7.4%; Score 105; DB 14; Length 6769;
Best Local Similarity 76.1%; Pred. No. 9,80e-50;
Matches 175; Conservative 0; Mismatches 52; Indels 3; Gaps 3;

Db 2790 GGAATTCAAGCCAGCCCTGCACCAACATGAGAAACCCCATCTCTACTTAAAAA
    ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Cp 1286 GGAATTGAGACCGACCCCTGCACCAACATGCGAAATGCGCATCTTACCAAAACAA
    ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Db 2850 AAAAATATAGCCGGGGTGGTGGCTTATGCTTATCCAGCTACTGAGAGGCTGAGGC
    ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Cp 1226 AAAAGTTAGTAGAGGTGAGTGGTGGCCCTTCTCTGTAGTTCAGACTTACT-AGGAGACTGAGGC
    ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Db 2910 AGGAGAAATCGCTTGAAAC-CCAGAGAAGCAGAGGTTGCAGGTGAGCCAAAGATCGCACCATTCG
    ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Cp 1167 AGGAGGATCACTTAGTGCCTCCAGAGGTCACAGAGTCGACAGAGCCATGGTGGTGCACATGCG
    ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Db 2969 ACTCCAGCCTTAGGCACACAGAGTGAACCTCATCTCAAAAAAAAAAAAAA 3018
    ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Cp 1107 ACTCCAGCCTGGGTGACA-GAGTGAGACCCCTGTCAAAAAAAAAAAAAA 1059
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RESULT      9
ID      US-08-480-784-20 STANDARD; DNA; UNC; 6769 BP.
AC      xxxxxx
DT      01-JAN-1900
DE      Sequence 20, Application US/08480784.
CC      Sequence 20, Application US/08480784
CC      Patent No. 5693473
CC      GENERAL INFORMATION:
CC      APPLICANT: Skolnick, Mark H.
CC      APPLICANT: Goldgar, David E.
CC      APPLICANT: Miki, Yoshio
CC      APPLICANT: Swenson, Jeff
CC      APPLICANT: Kamp, Alexander
CC      APPLICANT: Harshman, Kelch D.

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CC APPLICANT: Shattuck-Eldens, Donna M.
CC APPLICANT: Tavtavian, Sean V.
CC APPLICANT: Wiseman, Roger W.
CC APPLICANT: Futreal, P. Andrew
CC TITLE OF INVENTION: 17q-Linked Breast and Ovarian Cancer
CC TITLE OF INVENTION: Susceptibility Gene
CC NUMBER OF SEQUENCES: 85
CC CORRESPONDENCE ADDRESS:
CC ADDRESSEE: Venable, Baetjer, Howard & Civiletti, LLP
CC STREET: 1201 New York Avenue, N.W., Suite 1000
CC CITY: Washington
CC STATE: DC
CC COUNTRY: USA
CC ZIP: 20005
CC COMPUTER READABLE FORM:
CC MEDIUM TYPE: Floppy disk
CC COMPUTER: IBM PC compatible
CC OPERATING SYSTEM: PC-DOS/MS-DOS
CC SOFTWARE: Patentin Release #1.0, Version #1.30
CC CURRENT APPLICATION DATA:
CC APPLICATION NUMBER: US/08/480,784
CC FILING DATE:
CC CLASSIFICATION: 435
CC PRIOR APPLICATION DATA:
CC APPLICATION NUMBER: US 08/409,305
CC FILING DATE: 24-MAR-1995
CC PRIOR APPLICATION DATA:
CC APPLICATION NUMBER: US 08/348,824
CC FILING DATE: 29-NOV-1994
CC PRIOR APPLICATION DATA:
CC APPLICATION NUMBER: US 08/308,104
CC FILING DATE: 16-SEP-1994
CC PRIOR APPLICATION DATA:
CC APPLICATION NUMBER: US 08/300,266
CC FILING DATE: 02-SEP-1994
CC PRIOR APPLICATION DATA:
CC APPLICATION NUMBER: US 08/289,221
CC FILING DATE: 12-AUG-1994
CC ATTORNEY/AGENT INFORMATION:
CC NAME: Ihnen, Jeffrey L.
CC REGISTRATION NUMBER: 28,957
CC REFERENCE/DOCKET NUMBER: 24884-109347
CC TELECOMMUNICATION INFORMATION:
CC TELEPHONE: 202-962-4810
CC TELEFAX: 202-962-8300
CC INFORMATION FOR SEQ ID NO: 20:
CC SEQUENCE CHARACTERISTICS:
CC LENGTH: 6769 base pairs
CC TYPE: nucleic acid
CC STRANDEDNESS: double
CC TOPOLOGY: linear
CC MOLECULE TYPE: DNA (genomic)
CC HYPOTHEICAL: NO
CC ANTI-SENSE: NO
CC ORIGINAL SOURCE:
CC ORGANISM: Homo sapiens
CC SEQ Sequence 6769 BP; 1954 A; 1377 C; 1469 G; 1937 T; 32 other;

Query Match 7.4%; Score 105; DB 7; Length 6769;
Best Local Similarity 76.1%; Pred. No. 9,80e-50;
Matches 175; Conservative 0; Mismatches 52; Indels 3; Gaps 3;

Db 27190 GGAATTCAGACGACGCTGACCAACATGAGAAACCCCATCTCTACTAAACAAAAA 2849
Cc ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||
Cp 1286 GGAATTGAGACGACGCTGTACACACATGGCGAAATGCGATCTTTACCAACAAAAA 1227
Cc ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||
Db 2850 AAAAAATTAGCCGGGGTGTGGCTTAATGCTGTAAATCCAGCTACTCAGAGGCTGAGGC 2909
Cc ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||
Cp 12226 AAAAGTTAGTCAGGTGTGGTGGCCCTCTTGTAGTTCAGCTACT-AGGAGACTGAGGC 1168
Cc ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||
Db 29110 AGGAGATTCGCTTAAAC-CCAGAGAGAGAGGTTCGAGTGAAGCCAGAGATCGCACACATGC 2968
Cc ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||
Cp 1167 AGGAGGATCACTTATAGCTCCACAGAGGTCAAGGCTGACAGAGAGCATGCTGTGTCACCTGC 1108
Cc ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||

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Db 2969 ACTCCAGCTAGGACACAGAGTGAACCTCATCTCAAAAAAAAAAAAA 3018
CP 1107 ACTCCAGCTGGGTGACA-GAGTGAGACCTCTGCAAAAAAAAAAAAA 1059

RESULT 10

ID US-08-261-578-11 STANDARD; DNA; UNC; 2048 BP.
AC xxxxxx
DT 01-JAN-1900
DE Sequence 11, Application US/08261578.
CC Sequence 11, Application US/08261578
CC Patent No. 5491075
CC GENERAL INFORMATION:
CC APPLICANT: Desnick, Robert J.
CC APPLICANT: Bishop, David F.
CC APPLICANT: Ioannou, Yiannis A.
CC APPLICANT: Wang, Anne M.
CC TITLE OF INVENTION: CLONING AND EXPRESSION OF BIOLOGICALLY
CC TITLE OF INVENTION: ACTIVE ALPHA-N-ACETYLGLACTOSAMINIDASE
CC NUMBER OF SEQUENCES: 24
CC CORRESPONDENCE ADDRESS:
CC ADDRESSEE: PENNIE & EDMONDS
CC STREET: 1155 Avenue of the Americas
CC CITY: New York
CC STATE: New York
CC COUNTRY: U.S.A.
CC ZIP: 10036
CC COMPUTER READABLE FORM:
CC MEDIUM TYPE: Floppy disk
CC COMPUTER: IBM PC compatible
CC OPERATING SYSTEM: PC-DOS/MS-DOS
CC SOFTWARE: Patentin Release #1.0, Version #1.25
CC CURRENT APPLICATION DATA:
CC APPLICATION NUMBER: US/08/261,578
CC FILING DATE: '17-JUN-1994
CC CLASSIFICATION: 435
CC PRIOR APPLICATION DATA:
CC APPLICATION NUMBER: US 07/602,608
CC FILING DATE: 24-OCT-1990
CC ATTORNEY/AGENT INFORMATION:
CC NAME: Coruzzi, Laura A.
CC REGISTRATION NUMBER: 30,742
CC REFERENCE/DOCKET NUMBER: 6923-008
CC TELECOMMUNICATION INFORMATION:
CC TELEPHONE: (212) 790-9090
CC TELEFAX: (212) 869-8864/9741
CC TELEX: 66141 PENNIE
CC INFORMATION FOR SEQ ID NO: 11:
CC SEQUENCE CHARACTERISTICS:
CC LENGTH: 2048 base pairs
CC TYPE: nucleic acid
CC STRANDEDNESS: double
CC TOPOLOGY: unknown
CC MOLECULE TYPE: DNA (genomic)
CC Sequence 2048 BP; 457 A; 540 C; 552 G; 499 T; 0 other;

Query Match 7.3%; Score 103; DB 5; Length 2048;
Best Local Similarity 76.1%; Pred. No. 1,96e-48;
Matches 172; Conservative 0; Mismatches 51; Indels 3; Gaps 3;

Db 1058 TTTTGTGAGTGAAGAGTCTCAGCTGATGAGCCAGGCTGAGTGCAGCC 1117
Qy 1059 TTTTGTGAGTGAAGAGTCTCAGCTGATGAGCCAGGCTGAGTGCAGCC 1118
Db 1118 ATCTCAGCTCAGTCAACCTCTGCTCCAG-GTTCAGGATTTTCTCTCAGCTC 1176
Qy 1119 ACCATGGCTCTGCAAGCTCTGAGCTGAGTGCATCTCTCAGTCTC 1178
Db 1177 CCAGTAGCTGAGTGAAGAGTGTGGCCACACACCGGCTAATTTTGTATTTT 1236
Qy 1179 CTAG-TAGTGGAGTGAAGAGGAGGCGACACCTGACTTACTTTT-GTTTTTG 1236

Db 1237 TTCAGTAGAGACAGGGTTTCACATCTTGCCAGGCTACTCTAAA 1282
Qy 1237 TTTGTGAAGATGTCATTTGCGCATGTGTACAGGCTGGTCTCAA 1282

RESULT 11

ID US-07-602-608-11 STANDARD; DNA; UNC; 2048 BP.
AC xxxxxx
DT 01-JAN-1900
DE Sequence 11, Application US/07602608.
CC Sequence 11, Application US/07602608
CC Patent No. 5382524
CC GENERAL INFORMATION:
CC APPLICANT: Desnick, Robert J.
CC APPLICANT: Bishop, David F.
CC APPLICANT: Ioannou, Yiannis A.
CC APPLICANT: Wang, Anne M.
CC TITLE OF INVENTION: CLONING AND EXPRESSION OF BIOLOGICALLY
CC TITLE OF INVENTION: ACTIVE ALPHA-N-ACETYLGLACTOSAMINIDASE
CC NUMBER OF SEQUENCES: 24
CC CORRESPONDENCE ADDRESS:
CC ADDRESSEE: PENNIE & EDMONDS
CC STREET: 1155 Avenue of the Americas
CC CITY: New York
CC STATE: New York
CC COUNTRY: U.S.A.
CC ZIP: 10036
CC COMPUTER READABLE FORM:
CC MEDIUM TYPE: Floppy disk
CC COMPUTER: IBM PC compatible
CC OPERATING SYSTEM: PC-DOS/MS-DOS
CC SOFTWARE: Patentin Release #1.0, Version #1.25
CC CURRENT APPLICATION DATA:
CC APPLICATION NUMBER: US/07/602,608
CC FILING DATE: 24-OCT-1990
CC CLASSIFICATION: 435
CC ATTORNEY/AGENT INFORMATION:
CC NAME: Coruzzi, Laura A.
CC REGISTRATION NUMBER: 30,742
CC REFERENCE/DOCKET NUMBER: 6923-008
CC TELECOMMUNICATION INFORMATION:
CC TELEPHONE: (212) 790-9090
CC TELEFAX: (212) 869-8864/9741
CC TELEX: 66141 PENNIE
CC INFORMATION FOR SEQ ID NO: 11:
CC SEQUENCE CHARACTERISTICS:
CC LENGTH: 2048 base pairs
CC TYPE: nucleic acid
CC STRANDEDNESS: double
CC TOPOLOGY: unknown
CC MOLECULE TYPE: DNA (genomic)
CC Sequence 2048 BP; 457 A; 540 C; 552 G; 499 T; 0 other;

Query Match 7.3%; Score 103; DB 4; Length 2048;
Best Local Similarity 76.1%; Pred. No. 1,96e-48;
Matches 172; Conservative 0; Mismatches 51; Indels 3; Gaps 3;

Db 1058 TTTTGTGAGTGAAGAGTCTCAGCTGATGAGCCAGGCTGAGTGCAGCC 1117
Qy 1059 TTTTGTGAGTGAAGAGTCTCAGCTGATGAGCCAGGCTGAGTGCAGCC 1118
Db 1118 ATCTCAGCTCAGTCAACCTCTGCTCCAG-GTTCAGGATTTTCTCTCAGCTC 1176
Qy 1119 ACCATGGCTCTGCAAGCTCTGAGCTGAGTGCATCTCTCAGTCTC 1178
Db 1177 CCAGTAGCTGAGTGAAGAGTGTGGCCACACACCGGCTAATTTTGTATTTT 1236
Qy 1179 CTAG-TAGTGGAGTGAAGAGGAGGCGACACCTGACTTACTTTT-GTTTTTG 1236
Db 1237 TTCAGTAGAGACAGGGTTTCACATCTTGCCAGGCTACTCTAAA 1282
Qy 1237 TTTGTGAAGATGTCATTTGCGCATGTGTACAGGCTGGTCTCAA 1282

RESULT 12
ID PCT-US95-07201-10 STANDARD; DNA; UNC; 7210 BP.
AC xxxxxx
DT 01-JAN-1900
DE Sequence 10, Application PC/TUS9507201.
CC Sequence 10, Application PC/TUS9507201
CC GENERAL INFORMATION:
CC APPLICANT: Chader, Gerald J.; Becerra, Sofia
CC APPLICANT: Patricia; Schwartz, Joan P.;
CC APPLICANT: Taniwaki, Takayuki
CC TITLE OF INVENTION: PIGMENT EPITHELIUM
CC TITLE OF INVENTION: DERIVED FACTOR: CHARACTERIZATION GENOMIC
CC TITLE OF INVENTION: ORGANIZATION AND SEQUENCE OF THE PEDF GENE
CC NUMBER OF SEQUENCES: 43
CC CORRESPONDENCE ADDRESS:
CC ADDRESSEE: Morgan & Finnegan, L.L.P.
CC STREET: 345 Park Avenue
CC CITY: New York
CC STATE: New York
CC COUNTRY: USA
CC ZIP: 10154
CC COMPUTER READABLE FORM:
CC MEDIUM TYPE: Floppy Disk
CC COMPUTER: IBM PC Compatible
CC OPERATING SYSTEM: PC-DOS/MS-DOS
CC SOFTWARE: WORDPERFECT 5.1
CC CURRENT APPLICATION DATA:
CC APPLICATION NUMBER: PCT/US95/07201
CC FILING DATE: 06-JUN-1995
CC CLASSIFICATION:
CC PRIOR APPLICATION DATA:
CC APPLICATION NUMBER: 08/367,841
CC FILING DATE: 30-DEC-1994
CC PRIOR APPLICATION DATA:
CC APPLICATION NUMBER: 08/257,963
CC FILING DATE: 07-JUN-1994
CC PRIOR APPLICATION DATA:
CC APPLICATION NUMBER: 07/952,796
CC FILING DATE: 24-SEP-1992
CC ATTORNEY/AGENT INFORMATION:
CC NAME: DOROTHY R. AUTH
CC REGISTRATION NUMBER: 36434
CC REFERENCE/DOCKET NUMBER: 20264126PCT
CC TELECOMMUNICATION INFORMATION:
CC TELEPHONE: (212) 758-4800
CC TELEFAX: (212) 751-6849
CC INFORMATION FOR SEQ ID NO: 10:
CC SEQUENCE CHARACTERISTICS:
CC LENGTH: 7210 Base Pairs
CC TYPE: Nucleic Acid
CC STRANDEDNESS: Double
CC TOPOLOGY: Unknown
CC MOLECULE TYPE: Genomic DNA
CC ORIGINAL SOURCE:
CC ORGANISM: Human
CC IMMEDIATE SOURCE:
CC LIBRARY: DASH II
CC FEATURE:
CC NAME/KEY: JT6A
CC LOCATION:
CC IDENTIFICATION METHOD:
CC OTHER INFORMATION: 7.0 kb Not 1-Not
CC OTHER INFORMATION: fragment; derived from human placental
CC OTHER INFORMATION: genomic DNA; also referred to as JT106
SQ Sequence 7210 BP; 1878 A; 1688 C; 2052 G; 1592 T; 0 other;

Query Match 7.1%; Score 101; DB 14; Length 7210;
Best Local Similarity 76.2%; Pred. No. 3,91e-47;
Matches 176; Conservative 0; Mismatches 51; Indels 4; Gaps 4;

Db 6074 CTTTCTTTTGAAGCGGCTCTGTCGCCAGGATGAGTGCAGTGGTGT 6133
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QY 1058 CTTTCTTTTGAAGCGGCTCTGTCGCCAGGATGAGTGCAGTGGTGCAC 1117
Db 6134 GATCTAGCTCACTGCAACCTCCGCTCCAG-GTTAAAGTATTTCTGCTCGACACT 6192
QY 1118 CACCATGGCTCTCTGCGACCTCTGGAGCTCAAGTATCTCTGCTCGACT 1177
Db 6193 CCAAGTAGCTGGAGCTACAGGTGCGCCACACACCTGGTAATTTGTT-TGATTT- 6250
QY 1178 CTTA-GTAGCTGGAATCTACAGGAAGGCCACACCTGACTACTATTTTGTTTT 1236
Db 6251 TTTAGTAGAGATGGGTTTCCACCGTGTGACTGAGCTGCTGGAACCTCT 6301
QY 1237 TTTGTAAGATGATTCATTTGCGCATGTTGACAGGCTGGTCTAACTCCT 1287

RESULT 13
ID PCT-US95-07201-43 STANDARD; DNA; UNC; 22481 BP.
AC xxxxxx
DT 01-JAN-1900
DE Sequence 43, Application PC/TUS9507201.
CC Sequence 43, Application PC/TUS9507201
CC GENERAL INFORMATION:
CC APPLICANT: Chader, Gerald J.; Becerra, Sofia
CC APPLICANT: Patricia; Schwartz, Joan P.;
CC APPLICANT: Taniwaki, Takayuki
CC TITLE OF INVENTION: PIGMENT EPITHELIUM
CC TITLE OF INVENTION: DERIVED FACTOR: CHARACTERIZATION GENOMIC
CC NUMBER OF SEQUENCES: 43
CC CORRESPONDENCE ADDRESS:
CC ADDRESSEE: Morgan & Finnegan, L.L.P.
CC STREET: 345 Park Avenue
CC CITY: New York
CC STATE: New York
CC COUNTRY: USA
CC ZIP: 10154
CC COMPUTER READABLE FORM:
CC MEDIUM TYPE: Floppy Disk
CC COMPUTER: IBM PC Compatible
CC OPERATING SYSTEM: PC-DOS/MS-DOS
CC SOFTWARE: WORDPERFECT 5.1
CC CURRENT APPLICATION DATA:
CC APPLICATION NUMBER: PCT/US95/07201
CC FILING DATE: 06-JUN-1995
CC CLASSIFICATION:
CC PRIOR APPLICATION DATA:
CC APPLICATION NUMBER: 08/367,841
CC FILING DATE: 30-DEC-1994
CC PRIOR APPLICATION DATA:
CC APPLICATION NUMBER: 08/257,963
CC FILING DATE: 07-JUN-1994
CC PRIOR APPLICATION DATA:
CC APPLICATION NUMBER: 07/952,796
CC FILING DATE: 24-SEP-1992
CC ATTORNEY/AGENT INFORMATION:
CC NAME: DOROTHY R. AUTH
CC REGISTRATION NUMBER: 36434
CC REFERENCE/DOCKET NUMBER: 20264126PCT
CC TELECOMMUNICATION INFORMATION:
CC TELEPHONE: (212) 758-4800
CC TELEFAX: (212) 751-6849
CC INFORMATION FOR SEQ ID NO: 43:
CC SEQUENCE CHARACTERISTICS:
CC LENGTH: 22481 Base Pairs
CC TYPE: Nucleic Acid
CC STRANDEDNESS: Double
CC TOPOLOGY: Unknown
CC MOLECULE TYPE: Genomic DNA
CC FEATURE:
CC NAME/KEY: PL-147
CC LOCATION:
CC IDENTIFICATION METHOD:
CC OTHER INFORMATION: full length genomic

OTHER INFORMATION: sequence for PEDF plus flanking sequences.
 CC Sequence 22481 BP; 5280 A; 5708 C; 6136 G; 5347 T; 10 other;

Query Match 7.1%; Score 101; DB 14; Length 22481;
 Best Local Similarity 76.2%; Pred. No. 3.91e-47;
 Matches 176; Conservative 0; Mismatches 51; Indels 4; Gaps 4;

Db 6067 CTTTCTTTTGTGTAAGAGGGGCTCTCTCTGCGCCCAAGATGAGTGCATGGGTGT 6126
 OY TTTTCTTTTGTGTAAGAGGGGCTCTCTCTGCGCCCAAGATGAGTGCATGGGTGT 6117
 Db 6127 GATCTCAGCTCAGTCAACCTCCGCTCCAG-GTTTAAGTATCTCTGCTCAGACT 6185
 OY TTTTCTTTTGTGTAAGAGGGGCTCTCTCTGCGCCCAAGATGAGTGCATGGGTGT 6117
 Db 1118 CACATGCTCTCTGACCTTGTGAGCTCAAGTATCTCTGCTCAGTCT 1177
 OY TTTTCTTTTGTGTAAGAGGGGCTCTCTCTGCGCCCAAGATGAGTGCATGGGTGT 6117
 Db 6186 CCAAGTAGCTGGAGCTACAGTGGCGCCCAACACACCTGGGTAATTTGTT-TCATT- 6243
 OY TTTTCTTTTGTGTAAGAGGGGCTCTCTCTGCGCCCAAGATGAGTGCATGGGTGT 6117
 Db 1178 CCAAGTAGCTGGAGCTACAGTGGCGCCCAACACACCTGGGTAATTTGTT-TCATT- 6243
 OY TTTTCTTTTGTGTAAGAGGGGCTCTCTCTGCGCCCAAGATGAGTGCATGGGTGT 6117
 Db 6244 TTTAGTAGAGTGGGTTTCACCGCTGTGACTAGCTGTCTCCAGTCTCT 6294
 OY TTTTCTTTTGTGTAAGAGGGGCTCTCTCTGCGCCCAAGATGAGTGCATGGGTGT 6117
 Db 1237 TTTGTAAGATGGCATTTCCCATGTGTGACAGGCTGTCTCAAACTCCT 1287

RESULT 14
 ID US-08-370-975B-6 STANDARD; DNA; UNC; 20303 BP.
 AC xxxxxx
 DT 01-JAN-1900
 DE Sequence 6, Application US/08370975B.
 CC Sequence 6, Application US/08370975B
 CC Patent No. 5622851
 CC GENERAL INFORMATION:
 CC APPLICANT: Maley, Frank
 CC APPLICANT: Maley, Gladys F.
 CC APPLICANT: Weiner, Karen X.B.
 CC TITLE OF INVENTION: Human Deoxycytidylate Deaminase Gene
 CC NUMBER OF SEQUENCES: 14
 CC CORRESPONDENCE ADDRESS:
 CC ADDRESSEE: Nixon, Hargrave, Devans & Doyle
 CC STREET: Clinton Square, P.O. Box 1051
 CC CITY: Rochester
 CC STATE: New York
 CC COUNTRY: USA
 CC ZIP: 14603
 CC COMPUTER READABLE FORM:
 CC MEDIUM TYPE: Floppy disk
 CC COMPUTER: IBM PC compatible
 CC OPERATING SYSTEM: PC-DOS/MS-DOS
 CC SOFTWARE: Patentin Release #1.0, Version #1.25
 CC CURRENT APPLICATION DATA:
 CC APPLICATION NUMBER: US/08/370, 975B
 CC FILING DATE: 10-JAN-1995
 CC CLASSIFICATION: 435
 CC ATTORNEY/AGENT INFORMATION:
 CC NAME: Timian, Susan J.
 CC REGISTRATION NUMBER: 34,103
 CC REFERENCE/DOCKET NUMBER: 20894/80
 CC TELECOMMUNICATION INFORMATION:
 CC TELEPHONE: (716)263-1636
 CC TELEFAX: (716)263-1600
 CC INFORMATION FOR SEQ ID NO: 6:
 CC SEQUENCE CHARACTERISTICS:
 CC LENGTH: 20303 base pairs
 CC TYPE: nucleic acid
 CC STRANDEDNESS: single
 CC TOPOLOGY: linear
 CC MOLECULE TYPE: DNA (genomic)
 CC POSITION IN GENOME:
 CC CHROMOSOME/SEGMENT: 4q35
 CC Sequence 20303 BP; 5454 A; 4115 C; 5052 G; 5682 T; 0 other;
 Query Match 7.0%; Score 99; DB 7; Length 20303;
 Best Local Similarity 80.1%; Pred. No. 7.75e-46;

Matches 185; Conservative 0; Mismatches 38; Indels 8; Gaps 5;
 Db 6226 TTTTCTTTTGTGTAAGAGGGGCTCTCTCTGCGCCCAAGATGAGTGCATGGGTGT 6285
 OY TTTTCTTTTGTGTAAGAGGGGCTCTCTCTGCGCCCAAGATGAGTGCATGGGTGT 6118
 Db 6286 ATCTTGGCTCAGTCAACCTCCGCTCCAG-GTTTCAAGCATTTCTCTGCTCAGCTC 6344
 OY TTTTCTTTTGTGTAAGAGGGGCTCTCTCTGCGCCCAAGATGAGTGCATGGGTGT 6118
 Db 6345 GGAGTGTGTGATTTACAGAGCTGCGCCAGCGCTGTAA--TTTGTATTTT- 6401
 OY TTTTCTTTTGTGTAAGAGGGGCTCTCTCTGCGCCCAAGATGAGTGCATGGGTGT 6118
 Db 1179 CTAGTAGCTG-GA-ACACAGAGAGGGCCACACACCTGACTTATTTTGTGTTTGTG 1236
 OY TTTTCTTTTGTGTAAGAGGGGCTCTCTCTGCGCCCAAGATGAGTGCATGGGTGT 6118
 Db 6402 --TAGTAGAGATGGGTTTCACCATGTTGGCCAGGCTGTCTCAAACTCCT 6450
 OY TTTTCTTTTGTGTAAGAGGGGCTCTCTCTGCGCCCAAGATGAGTGCATGGGTGT 6118
 Db 1237 TTTGTAAGATGGCATTTCCCATGTGTGACAGGCTGTCTCAAACTCCT 1287

RESULT 15
 ID US-08-370-975B-1 STANDARD; DNA; UNC; 26764 BP.
 AC xxxxxx
 DT 01-JAN-1900
 DE Sequence 1, Application US/08370975B.
 CC Sequence 1, Application US/08370975B
 CC Patent No. 5622851
 CC GENERAL INFORMATION:
 CC APPLICANT: Maley, Frank
 CC APPLICANT: Maley, Gladys F.
 CC APPLICANT: Weiner, Karen X.B.
 CC TITLE OF INVENTION: Human Deoxycytidylate Deaminase Gene
 CC NUMBER OF SEQUENCES: 14
 CC CORRESPONDENCE ADDRESS:
 CC ADDRESSEE: Nixon, Hargrave, Devans & Doyle
 CC STREET: Clinton Square, P.O. Box 1051
 CC CITY: Rochester
 CC STATE: New York
 CC COUNTRY: USA
 CC ZIP: 14603
 CC COMPUTER READABLE FORM:
 CC MEDIUM TYPE: Floppy disk
 CC COMPUTER: IBM PC compatible
 CC OPERATING SYSTEM: PC-DOS/MS-DOS
 CC SOFTWARE: Patentin Release #1.0, Version #1.25
 CC CURRENT APPLICATION DATA:
 CC APPLICATION NUMBER: US/08/370, 975B
 CC FILING DATE: 10-JAN-1995
 CC CLASSIFICATION: 435
 CC ATTORNEY/AGENT INFORMATION:
 CC NAME: Timian, Susan J.
 CC REGISTRATION NUMBER: 34,103
 CC REFERENCE/DOCKET NUMBER: 20894/80
 CC TELECOMMUNICATION INFORMATION:
 CC TELEPHONE: (716)263-1636
 CC TELEFAX: (716)263-1600
 CC INFORMATION FOR SEQ ID NO: 1:
 CC SEQUENCE CHARACTERISTICS:
 CC LENGTH: 26764 base pairs
 CC TYPE: nucleic acid
 CC STRANDEDNESS: single
 CC TOPOLOGY: linear
 CC MOLECULE TYPE: DNA (genomic)
 CC POSITION IN GENOME:
 CC CHROMOSOME/SEGMENT: 4q35
 CC Sequence 26764 BP; 7079 A; 5521 C; 6539 G; 7625 T; 0 other;
 Query Match 7.0%; Score 99; DB 7; Length 26764;
 Best Local Similarity 80.1%; Pred. No. 7.75e-46;
 Matches 185; Conservative 0; Mismatches 38; Indels 8; Gaps 5;
 Db 8189 TTTTCTTTTGTGTAAGAGGGGCTCTCTCTGCGCCCAAGATGAGTGCATGGGTGT 8248
 OY TTTTCTTTTGTGTAAGAGGGGCTCTCTCTGCGCCCAAGATGAGTGCATGGGTGT 1118

Thu Mar 26 09:16:05 1998

US-08-236-918A-7.rni

Page 12

Db	8249	ATCTTGGCTACATCAGCACCACCTCCACAGTT-TCAGAGATTCTCGTCTAGCCTC	8307
Qy	1119	ACCATGCTCTCTCCACCTTGACCTTGGAGCTCAAGTGTATCCCTCGCTCAGTTC	1178
Db	8308	GGATGACGTGTGATTACAGAGCAGCGCCACGACCGTGA-TTTTGTATTTT-	8364
Qy	1179	CTAGTAGTG-GA-ACTCAGAAGAGGGCCACACACCTGACACTTTTGTGTTTTTG	1236
Db	8365	-TATGATGAGATGGGTTTTACCATGTTGGCCAGCGTGTCTCAACTCCT	8413
Qy	1237	TTTGTAAGATGCGCATTTTGGCCATGTGTGACAGCGTGGTGTCAACTCCT	1287

Search completed: Wed Mar 25 14:05:28 1998
Job time : 94 secs.



Release 2.1D John F. Collins, Biocomputing Research Unit.
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Msrch_un n.a. - n.a. database search, using Smith-Waterman algorithm
Run on: Wed Mar 25 13:29:04 1998; Maspar time 175.73 Seconds
929.178 Million cell updates/sec
Near output not generated.

Title: >US-08-236-918A-7
Description: (1-1415) from 5674704.seq
Perfect Score: 1415
N.A. Sequence: 1 AGTGGAAAGTCTCCGGCAG.....TCATTAATTTTATTTTATTTT
Comp: TCACCTTCAAGAGCGCGTC.....ACATTTTATTTTATTTTATTTT

Scoring table: TABLE default
Gap 6

Nmatch STD : Dbase 0; Query 0

Searched: 159651 seqs, 5769862 bases x 2

Post-processing: Minimum Match 0%
Listing first 45 summaries

Database:

n-geneseq30
1:part1 2:part2 3:part3 4:part4 5:part5 6:part6 7:part7
8:part8 9:part9 10:part10 11:part11 12:part12 13:part13
14:part14 15:part15 16:part16 17:part17 18:part18
19:part19 20:part20 21:part21 22:part22 23:part23
24:part24 25:part25 26:part26 27:part27 28:part28
29:part29 30:part30 31:part31 32:part32 33:part33

Statistics: Mean 9.526; Variance 6.639; scale 1.435

Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Match	Length	DB	ID	Description	Pred. No.
1	1415	100.0	1415	13	075424	Human 4-1BB polypept	0.00e+00
2	1390	98.2	1439	15	092086	Human 4-1BB polypept	0.00e+00
3	836	59.1	838	14	086126	Human 4-1BB polypept	0.00e+00
4	834	58.9	838	24	139541	Human 4-1BB polypept	0.00e+00
5	233	16.5	2347	24	139541	Human 4-1BB polypept	0.00e+00
6	231	16.3	2350	14	086127	Human 4-1BB polypept	0.00e+00
7	229	16.2	768	13	075428	Human 4-1BB polypept	0.00e+00
8	114	8.1	2649	6	035034	Human 4-1BB polypept	0.00e+00
9	108	7.6	4359	14	045625	Human 4-1BB polypept	0.00e+00
10	108	7.6	11298	33	086756	Human 4-1BB polypept	0.00e+00
11	108	7.6	11357	9	051024	Human 4-1BB polypept	0.00e+00
12	105	7.4	24025	21	171515	Human 4-1BB polypept	0.00e+00
13	105	7.4	24025	21	171515	Human 4-1BB polypept	0.00e+00
14	105	7.4	24026	21	171516	Human 4-1BB polypept	0.00e+00
15	105	7.4	24026	21	171516	Human 4-1BB polypept	0.00e+00

16	105	7.4	24026	21	171522	Mutated BRCA1 genomic	1.93e-42
17	105	7.4	24026	21	171517	Mutated BRCA1 genomic	1.93e-42
18	105	7.4	24026	21	171521	Mutated BRCA1 genomic	1.93e-42
19	105	7.4	24026	21	171526	Mutated BRCA1 genomic	1.93e-42
20	105	7.4	24026	21	171530	Mutated BRCA1 genomic	1.93e-42
21	105	7.4	24026	21	171514	Mutated BRCA1 genomic	1.93e-42
22	105	7.4	24026	21	171513	Mutated BRCA1 genomic	1.93e-42
23	105	7.4	24026	21	171528	Mutated BRCA1 genomic	1.93e-42
24	105	7.4	24026	21	171518	Mutated BRCA1 genomic	1.93e-42
25	105	7.4	24026	21	171512	Mutated BRCA1 genomic	1.93e-42
26	105	7.4	24026	21	171523	Mutated BRCA1 genomic	1.93e-42
27	105	7.4	24026	21	171519	Mutated BRCA1 genomic	1.93e-42
28	105	7.4	24026	21	171524	Mutated BRCA1 genomic	1.93e-42
29	105	7.4	24026	18	171525	Mutated BRCA1 genomic	1.93e-42
30	105	7.4	24026	21	171527	Mutated BRCA1 genomic	1.93e-42
31	105	7.4	24026	23	171512	Mutated BRCA1 genomic	1.93e-42
32	105	7.4	24026	21	171520	Mutated BRCA1 genomic	1.93e-42
33	105	7.4	24031	21	171525	Mutated BRCA1 genomic	1.93e-42
34	104	7.3	230	8	095868	Human brain expressed	2.67e-41
35	103	7.3	2045	4	025165	Genomic alpha-GalNAc	7.18e-42
36	104	7.3	6511	14	095493	Human Cdn-2 DNA	7.18e-42
37	101	7.1	22481	24	171558	PEPF full length sequ	3.68e-40
38	99	7.0	2435	23	173155	Tissue plasminogen ac	5.04e-39
39	99	7.0	20303	30	171699	Human deoxyribidylate	5.04e-39
40	99	7.0	26764	30	171696	Human deoxyribidylate	5.04e-39
41	97	6.9	392	8	060438	Human brain expressed	6.88e-38
42	97	6.9	2362	26	1748098	Human interleukin-12	6.88e-38
43	97	6.9	19012	6	023586	Natural killer cell s	6.88e-38
44	98	6.9	19012	6	023586	Sequence encoding hum	1.86e-38
45	96	6.8	5108	2	N60388	Sequence encoding hum	2.54e-37

ALIGNMENTS

RESULT 1	ID	075424	standard: cDNA to mRNA; 1415 BP.
AC	075424	08-AUG-1995 (first entry)	
DE	Human 4-1BB polypeptide coding sequence.		
KW	T-cell; lymphocyte; activation; tissue culture; clone; cell lines;		
OS	proliferation; stimulation; 4-1BB-L; ligand; receptor; cytokine; ss.		
OS	Homo sapiens.		
FT	Key	Location/Qualifiers	
FT	CDS	120..887	
FT	/product= a	4-1BB polypeptide.	
FT	sig-peptide	120..188	
FT	/tag= b	189..884	
FT	mat-peptide		
FT	/tag= c		
PN	WC09426290-A.		
PD	24-NOV-1994.		
PF	06-MAY-1994; U05036.		
PR	07-MAY-1993; US-060843.		
PA	(IMNV) IMMUNEX CORP.		
PI	Alderson MR, Goodwin RG, Smith CA;		
DR	WPI: 95-02265/03.		
DR	P-PSDB: R64197.		
PT	Cytokine, 4-1BB ligand (4-1BB-L) - binds to cell surface receptor		
PT	4-1BB to transduce signal		
PS	Claim 29; Page 46-47; 65pp; English.		
CC	The 4-1BB polypeptide (receptor) and the 4-1BB-L (cytokine, see		
CC	075423) are useful in a pharmaceutical composition for stimulating		
CC	the immune system. The 4-1BB and 4-1BB-L polypeptides are also useful		
CC	for exploring mechanisms of T-cell activation, as they are expressed		
CC	on T lymphocytes. 4-1BB-L can be used as a tissue culture reagent for		
CC	in vitro cultivation of primary T-cells during the derivation of		
CC	clonal T-cell lines. It may also be used to stimulate proliferation		
CC	of activated T-cells, used in therapeutic procedures. 365 T;		
CC	Sequence 1415 BP; 385 A; 332 C; 333 G;		
CC	Query Match 100.0%; Score 1415; DB 13; Length 1415;		
CC	Best Local Similarity 100.0%; Pred. No. 0.00e+00;		

Matches 1415; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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Db 1 agtggaaagtctccggagcccttgagatctcaagatgacattgttagaccagctat 60
QY 1 AGTGGAAAGTTCTCCGGAGCCCTGAGATCTCAAGATGACATTTGTAGACCCACTAT 60
Db 61 ttgataaatctctcttgaaatcaagcttctgtagatcatatccctgtgcagattcata 120
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Db 121 tgggaacagctgttacaacatagtagcaactgtgtgctgctcacaatttgaagga 180
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Db 181 caagatctcagagatctctgttagtaactcccaagctgtagacatctcgtataataca 240
QY 181 CAAGATCTCTCAGAGATCTTGTAGTAAGTCCAGCTGTGATCATCTGTGATTAATCA 240
Db 241 ggaatcaagattgcaagctccctgctcccaaatagttctccagcgaggtgacaaagga 300
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Db 301 ccgtgacatacagcagcagtgtaaggtgtttcaggaacaggaagagtgctccca 360
QY 301 CCTGTGACATATGACAGCAGTGTAAAGGTGTTTCAAGACAGAGAGAGTGTCTCCA 360
Db 361 ccagcaatgcagagatgtgactgcaactccaaggttctcagctggtggcagagatgcga 420
QY 361 CCAGCAATGCAGAGATGTACTGCACTCCAGGTTTCACTGCTGGGGCAGAGATGCACGA 420
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QY 421 TGTGTGAACAAGATGTGAACAAGGTACAGACTGACAAAAAGGTTGTAAAGACTTT 480
Db 481 gcttggagacattaaacatcagaagcgtggacatcgtcgaacctggaacactgttctt 540
QY 481 GCTTGGAGACATTTAAACATCAGAAACGTGGCATCTGTGACCCCTGACAAACTGTCTT 540
Db 541 tggatggaaaatctgctgtgtgtgaatggagaaagagagagctgtgtctgtgacat 600
QY 541 TGGATGGAAGATCTGTGCTGTGTGAATGGAGAAAGAGAGACCTGTGTGACCAT 600
Db 601 ctccagccagactctctccggagagacatcctctgtgacccgcctgcccctgcagagagc 660
QY 601 CTCACGCCGACTCTCTCCGGAGACATCTCTGTGATCCCGCTCCCTGCGAGAGAGC 660
Db 661 caggacactctccgcaagatcactctctctctctgtcgctgacgtgcagctgtgtctct 720
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QY 721 TCTCGTGTCTTCTCTCAGCTCCGCTTCTCTGTGTAAACGGGGCGAGAAAGAACTCC 780
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QY 781 TGTATATATTAACAACCAATTTATGAGACCAATGTAACACTACTMAAGAGATGCTCT 840
Db 841 gtaactgcagattccagaaagaaagagagatgtgaaactgtgaatgtgaatgcatt 900
QY 841 GTACTGCCGATTTCCAGAAAGAAAGAGAGATGTGAATGTGAATGTGAATGCAT 900
Db 901 aggcctgttggactctcttgaagaagaaagaaatataatgatacgcgtatcaagc 960
QY 901 AGGCTGTGGACTCTCTTGAAGAAGAAAGCAAGAAATATAGTATCCGTATCACAGC 960
Db 961 tttaaaagcagaacacactcctaataataacagagatcccccacaagcttctt 1020
QY 961 TTTAAAGCAGAAACACATCTCAATTAATCCAGGATTCCTCCCAACACAGCTTCTT 1020
Db 1021 tctaattgcacatagtgagctttaaataatgcacacttttttttttttttttgaag 1080
QY 1021 TCTAATGCCAATAGTGTGGCTTTAAATAATGCACACTTTTTTTTTTGTGTGACAG 1080

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Db 1081 gttcactctgtcaccagctgtgagtcagtggtgcacacatgtcctctgcagcttg 1140
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Db 1141 acccttggagactcaatgtatccctccctcagctcactccttagtagctggaactaagga 1200
QY 1141 ACCCTGGAGACTCAATGATCCCTCCGCTCACTCTCTAGTAGCTGGAACATCAAGGA 1200
Db 1201 aggcacacacactgtactaactttttgtttttgtttgttgaagatgacattgcga 1260
QY 1201 AGGCACACACACTGTACTAATCTTTTGTGTTTGTGTTAAAGATGCGATTTCCCA 1260
Db 1261 tttgtacagagctgtgtcaaacctcagatgtacacttgcctcccaagtgctggagt 1320
QY 1261 TTTGTACAGGCTGTGTCAAACTCTTAGGTTCACTTTGGCTCCAAAGTGTGGGATT 1320
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QY 1321 ACAGACATGAACCTCCAGCGCCGCCCAAAATATGCAACACTTTTAACAGACAGACA 1380
Db 1381 tgaggacagagctgtgtataaaaaaaaaaaaaa 1415
QY 1381 TGAGGACAGAGCTGTGTATAAAAAAAAAAAAAA 1415

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RESULT 2

ID 092086 standard; DNA; 1439 BP.

AC 092086;

DT 21-JAN-1996 (first entry)

DE Human receptor induced by lymphocyte activation (ILA) DNA.

KW ILA; receptor induced by lymphocyte activation; disease diagnosis;

OS Homo sapiens.

FN Key location/Qualifiers

FT CDS 140..904

PN /*tag- a

PD 28-MAR-1995. CA2108401-A.

PE 14-OCT-1993; 108401.

PR 27-SEP-1993; US-127693.

PA (REGC) UNIV CALIFORNIA.

PI Lotz M, Schwarz H.

DR WPI: 95-194420/26.

DR P-PSDB: R74087.

PT New receptor inducible by lymphocyte activation - used to develop

PT prods. for the diagnosis and treatment of inflammatory host defence

PT pathology.

PS Claim 52; Page 61; 91pp; English.

CC This DNA may be expressed recombinantly for the production of ILA.

CC The cDNA was isolated from a library constructed from activated

CC human T-lymphocyte leukemia virus type-1 transformed human T-

CC lymphocytes.

SQ Sequence 1439 BP; 393 A; 336 C; 346 G; 364 T;

Query Match 98.2%; Score 1390; DB 15; Length 1439;

Best Local Similarity 99.4%; Pred. No. 0.00e+00;

Matches 1408; Conservative 0; Mismatches 6; Indels 2; Gaps 2;

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Db 21 agtggaaagtctccggagcccttgagatctcaagatgacattgttagaccagctat 80
QY 1 AGTGGAAAGTTCTCCGGAGCCCTGAGATCTCAAGATGACATTTGTAGACCCACTAT 60
Db 81 ttgataaatctctcttgaaatcaagcttctgtagatcatatccctgtgcagattcata 140
QY 61 TTGATTAATAATCTCTTGTGAATCAAGCTTGTGATATCATACCTGTGCAATTTATCA 120
Db 141 tgggaacagctgttacaacatagtagcaactgtgtgctgctcacaatttgaagga 200
QY 121 TGGGAAACAGCTGTACACATAGTAGCACCTGTGCTGCTCCTCAACTTTGAGAGGA 180
Db 201 caagatctcagagatctctgttagtaactcccaagctgtagacatctcgtataataca 260

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QY 181 CAAGATCATGAGGATCCTTGTAGTAAGTCCGACGTGTAACATTTCTGTATATAACA 240
 Db 261 ggaatcagatttgcagtccttgcctcccaaatagtttctccagcaggtgagcaaaagga 320
 QY 241 GGAATCAGATTGTGAGTCCCTGCTCCCAAAATAGTTTCTCCAGCCAGAGTGAGCAAAAGGA 300
 Db 321 ccttgcagatttgcagaggaagtgttaaggtgttttccagagccagaggaagtgttcttcca 380
 QY 301 CCTGAGCATATGACAGGAGTGTAAAGGTGTTTTCAGAGCCAGGAGAGAGTGTCTCTCCA 360
 Db 381 ccagcaatgcagagtgatgcagtcagtcagaggtttccagtggtggtgggcaagatgcagca 440
 QY 361 CCAGCAATGCAGAGTGTGATCTGATCCAGAGTTTCACTGCTGGGGCAGAGATGCACAGA 420
 Db 441 tctgtcaagcagagattgttagacaaggltcaagaactgcacaaaaaaggtgttaagaactgt 500
 QY 421 TGTGTGACAGAGATGTAAACAGAGTCAAGAACTGACAAAAAAGGTTGTAAAGACTGTT 480
 Db 501 gctttggagacttttaagaatcaagaacgttgacatctgtccagccctgcagcaaacgttctt 560
 QY 481 GCTTTGGAGACTTTAAACATCAGAAACGTGACATCTGTGACCCCTGGACAAACTGTTCTT 540
 Db 561 tggatggaagaatctgtgtgttgaatggagcaagaagagagagctgtgtgtgtgagcat 620
 QY 541 TGGATGGAAGATCTGTGCTGTGTGAATGGGACGAGAGAGAGAGACTGGTCTGTGTGACCAT 600
 Db 621 ctcaagccagactctctccggagagacatctctgtgacgcgccttccctcgcagagagac 680
 QY 601 CTCAGCCGAGACTCTCTCCGGGAGGATCCTGTGTGACCCCGCTCCCTCGGAGAGAGAC 660
 Db 681 cagagacactctccgagatcatctcttcttctgtgcgtgagcgtgcagctgtgtctct 740
 QY 661 CAGGACACTCTCCGAGATCATCTCTTCTTCTGCGCTGACGCTGAGCTGCTGCTGCT 720
 Db 741 tccgtgttcttctccagcgtccgttctctgtgtgttaaacggcgagaaagaaccc 800
 QY 721 TCCGTGCTTCTTCTCCAGCTCCGCTTCTCTGTGTGTAAGGGGGCAGAAAGAACTCC 780
 Db 801 tctatatactcaaaacacatttaagacagcagtaacactcaacactcaagaagaagtgc 860
 QY 781 TGTATATATTTCAAAACACATTATGAGACCAAGTAACTCTAAAGAGAGAGTGGCT 840
 Db 861 gtaagtcgcgaattccagaagaagaagaagaagtgtgaactgtgaatgtgaatgtgaat 920
 QY 841 GTAGCTGCCGATTTTCCAGAGAAAGAAAGAGATGTGAATGTGAATGTGAATGTGAAT 900
 Db 921 agggctgtgtgagacttcttgaagaagaagaagaagaatgagatccgtctatcaacgc 980
 QY 901 AGGGCTGTGGGACTTTTCTGAAAAGAAAGCAAGAAATATGAGTATCCGCTATACAGC 960
 Db 981 ttcaaaagcaagaacacacatctctataataacccagagattccccaacacacagttctt 1040
 QY 961 TTTCAAAAAGCAAGAACACCATCTCTATATATACCAAGATTTCCCAACACACAGTTCTTT 1020
 Db 1041 tctaaatgcgaatgagctgtgaccttaaaaaatgacacacttcttcttcttggacag 1100
 QY 1021 TCTAAATGCCAATGAGTGTGGCTTAAATAATGACACACTTTTCTTTTATGACAGG 1080
 Db 1101 gttcactcctgtcaaccagagctgtgagtgcaatgacacacagagctctgcagccttg 1160
 QY 1081 GTTCACACTCTACCCAGGCTGGAGTGTGAGGACACCATGCTCTGTGACACCTTGG 1140
 Db 1161 acccttggagactcaagagatccctctcctcagatctcctgtgagctggagactcaagg 1220
 QY 1141 ACCTCTGGGAGCTCAAGATGATCTCTCTGCTCAGTCTCTCT -AGTAGCTGGAATCTCAAGG 1199
 Db 1221 aagggtccacacacactgacacttcttcttcttcttcttcttcttcttcttcttcttct 1279
 QY 1200 AAGGGCCACACACACTGATCACTTTTGTGTTTGTGTTTGTGTTTGTGTTTGTGTTTGTG 1259
 Db 1280 atgtgtatcagagctgtgtctcaaacctcaggttcaacttggccttcccaagtgtcggat 1339
 QY 1260 ATGTGTATCAGAGCTGTGCTCAAAACTCTAGTGTCTTGTGCTCTCCCAAAAGTGTGGAT 1319

Db 1340 tacagacatgaacttgcagagcccgcccaaaataatgacacactttaaagacagacag 1399
 QY 1320 TACAGACATGAACATGCCAGCCCGCCCAAAATATGACACCACTTTTAAAGACAGACAG 1379
 Db 1400 atgagagacagagctgtgtatataaaaaaaaaaaaaa 1435
 QY 1380 ATGAGGACAGAGCTGTGTGATATAAAAAAAAAAAAAA 1415
 RESULT 3
 ID Q86126 standard; cDNA: 838 BP.
 AC Q86126;
 DT 16-OCT-1995 (first entry)
 DE H4-1BB receptor protein cDNA.
 KW H4-1BB; receptor protein; immunosuppressive; autoimmune disease;
 KW organ transplantation; cell membrane ligand; ss.
 OS Homo sapiens.
 FH Key Location/Qualifiers
 FT CDS 41..808
 FN /*tag- a
 PM WO9507984-A.
 PD 23-MAR-1995.
 PE 15-SEP-1994; U10457.
 PR 16-SEP-1993; US-122796.
 PA (INDV) UNIV INDIANA FOUND.
 PI KWON BS;
 DR WPI: 95-131352/17.
 DR P-PSDB: R70977.
 PT Novel cDNA encoding human receptor protein H4-1BB - useful to
 PT produce the protein which is used to treat auto-immune disease
 PT and facilitate organ transplantation
 PS Claim 2; Fig.2; 36pp; English.
 CC Human peripheral blood lymphocyte-derived cDNA was amplified by PCR
 CC using probes based on the mouse receptor protein 4-1BB gene. The PCR
 CC product was used to screen a cDNA library of activated human T-cells.
 CC The isolated cDNA (Q86126), deposited as NRRL B21131, encoded the
 CC human homology, H4-1BB (R70977), of 4-1BB.
 SQ Sequence 838 BP; 218 A; 191 C; 215 G; 214 T;
 Query Match 59.1%; Score 836; DB 14; Length 838;
 Best Local Similarity 99.9%; Pred. No. 0.00e+00;
 Matches 837; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
 Db 1 aataagcttctgtatcatatcactgtgacagatttccatggaacagactgttaca 60
 QY 80 AATCAGCTTGTGTATCATATCCTGTGTCAGATTTCTATCATGGAACACACTGTTACAA 139
 Db 61 catagtagcacactgttctgtcttcccaacttgaagagacaagatcatgtcagagatcc 120
 QY 140 CATAGTAGCCACTGTGCTGCTGCTGCTCACTTTGAGAGGACAGATCATGTGACAGATCC 199
 Db 121 ttgtaagtaactgcagagctgtgtacattctgtgataataacaggaatcagattgcagtc 180
 QY 200 TTGTAGTAACTGCCCAGCTGCTGATCTGTGATATTAACAGGAATCAGATTGCAATGCC 259
 Db 181 ctgtccctccaataagtttcttccagcgagctgtgacaaagagcctgtgcataatgcagga 240
 QY 260 CTGTCTCTCAAAATAGTGTCTCCAGCGCAGGTGACAAAGGACCTGTGCATATCCAGGCA 319
 Db 241 gtgtaaaagtgttccaagacagaagaagtgttccccaacccaagatgagagtgga 300
 QY 380 CTGCACCTCAAGGTTTCACTGCTGGGGGAGATGACAGCATGTGTGAACAGGATTTGTA 439
 Db 361 acaaggttaagaacttgacaaaaaagaagtgtgaagacagctgtgttggagacatttaaga 420
 QY 440 ACAAGGTCTAAAGCTGACAAAAAAGGTTGTAAAGACGTGTGTTGGGACATTTAAGA 499
 Db 421 tcagaacagtgcatctgtcagacctggaacaactgttcttggatggaagagctgtgct 480

QY 500 TCAGAAAGTGGACATCTCTGACCTGACAAACTGTTCTTGGATGGAAAGTGTGTCT 559
DB 481 tctgaatggagcagaagagagagagcgtgtctgtggaacatctccagctgacctctcc 540
QY 560 TGTGAATGGAGCAGAGAGAGAGAGTGTGTGTGACCATCTCCAGCGACTCTCTCC 619
DB 541 gggagcaccctctgtgaccgccctgcccctgtgagagagcagacacctcccgcaat 600
QY 620 GGGAGCATCTCTGTGACCCCGCTGCCCTGTGAGAGAGCGAGACCTCTCCGCAAT 679
DB 601 catctcctctctctgtgctgacgtcagctcgtctgtctctctctctctccac 660
QY 680 CATCTCCTCTCTTCTTGTGGCGTGCAGCTGACGTGCTCTCTCCGCTTCTCTCAC 739
DB 661 gctccgttctctgtgtttaaagcgaggcagaagaactcctgtatataatcaaacacc 720
QY 740 GCTCGTTCTCTGTGTAAACGGGGCAGAAAGAACTCCGTATATATCAACAACAC 799
DB 721 attatgagaccagtaacaaactactcaagaagaatggtctgtagctccgattccaga 780
QY 800 ATTATGAGACCACTACAACTACTCAAGAGAGATGGCTGTAGCTGCCGATTTCCAGA 859
DB 781 agaagaagaagagagatgtgaactgtgaatggaagtcataaggcgtgtggaactt 838
QY 860 AGAAGAAGAAGAGAGATGTGAACCTGTGAATGGAAGTCAATAGGGCTGTGGACTTT 917

RESULT 4
ID T39546 standard; cDNA to mRNA; 838 BP.
AC T39546;
DT 12-DEC-1996 (first entry)
DE Human receptor H4-1BB cDNA.
KW Receptor 4-1BB; H4-1BB; monoclonal antibody; T-lymphocyte; T-cell;
KW Immunostimulant; cancer; autoimmune disease; graft rejection;
KW therapy; ss.
OS Homo sapiens.
FH Key Location/Qualifiers
FT CDS 41..808
FT /tag- a
FT mat_peptide 41..805
FT /tag- b
PN MO629348-A1.
PD 26-SEP-1996.
PF 22-MAR-1996; U03965.
PR 23-MAR-1995; US-409851.
PI (INDV) UNIV INDIANA FOUND.
PA Kang C, Kwon BS;
PI WPI: 96-443138/44.
P-SDS: W04174.
PT Monoclonal antibody specific for human receptor protein 4-1BB - used
PT to enhance proliferation and activation of T-cells for treatment of
PT cancer and to inhibit specific ligand binding for treating
PT auto-immune diseases
PS Disclosure: Page 36-37: 48pp; English.
CC A cDNA clone (T39546) codes for novel human receptor protein
CC H4-1BB (W04174), a protein that has the potential to function as
CC an accessory signaling molecule during T-cell activation and
CC proliferation. The cDNA clone was isolated from a lambda gtl1
CC cDNA library of activated human T lymphocytes by screening with a
CC PCR product obtd. by amplification of lymphocyte cDNA using
CC primers (see also T39542-45) based on the murine 4-1BB cDNA
CC (T39541). It can be used to produce recombinant H4-1BB useful
CC for isolating H4-1BB ligands, for stimulating proliferation of
CC B-cells expressing H4-1BB ligands, for blocking H4-1BB ligand
CC binding and for raising anti-H4-1BB monoclonal antibody.
SQ Sequence 838 BP; 218 A; 192 C; 214 G; 214 T;

Query Match 58.9%; Score 834; DB 24; Length 838;
Best Local Similarity 99.8%; Pred. No. 0.00e+00;
Matches 836; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

DB 1 atcagcttctgtatcatcacccgtgtccagatctcatcatcattggaaacagctgttaca 60

QY 80 AATCAGCTTCTAGTATACATACCTGTGCCAGATTTCATATGGAAACAGCTTTACAA 139
DB 61 catgttagcacctctgttctgtgtccctcaacttgagaagacaatcatatgcagatcc 120
QY 140 CATAGTAGCCACTCTGTGTGCTGCTCAACTTACATTGAGAGGACAAGATCATTCGAGATCC 199
DB 121 ttgtagaatgagcccaagctgtgtatattctgtgataataacaggaatcagattccagtc 180
QY 200 TTGTATGTAAGTCCCAAGTGTGTATCTTGTGTATATACAGAAATCAGATTTCAGATCC 259
DB 181 ctgtcctcccaatagtttctcctcagcgaggtgacaaagacccgtgtacatatgcagca 240
QY 260 CTGTCTCTCAATATGTTTCTCTCAGCGAGGTGACAAAGACCTGTGACATATTCAGAGCA 319
DB 241 gttgaagagtttctcagaccagaagagtgcttcctccacgaatgcagagtgtga 300
QY 320 GTGTAAAGTGTTTTTCAGGACACAGAGAGATGTCTCTCCACCGCAATGACAGATGTGA 379
DB 301 ctgacatccagaggtttcaactctctgaggggcagagtgagcaatgtgtgaacagattgaa 360
QY 380 CTGCATCTCAGAGTTTCACTGCTGTGGGGCAGATGCGATGTGTGACAGATTTGTAA 439
DB 361 acaaggtcaagaactgacaaacaaagggttgtaagactgtgtctgttggaacattaaaga 420
QY 440 ACAAGGTCAAGACTGACCAAAAAAGTTGTAAAGACTGTTGCTTTGGACATTTAACGA 499
DB 421 tcagaagaatgtgacatctgtgcacccctgcacaaactgttcttggatggaagtctgtgct 480
QY 500 TCAGAAAGTGGACATCTGTGACCCCTGAGCAAACTGTTGATGGAAGTGTGTGCT 559
DB 481 tgtgaatggagcagaagagagagagcgtgtgtgtgagacatctcagctgacctctcc 540
QY 560 TGTGAATGGAGCAGAGAGAGAGAGTGTGTGTGAGACATCTCAGCGACTCTCTCC 619
DB 541 gggagcaccctctgtgaccgccctgcccctgtgagagagcagaacactcccgcaat 600
QY 620 GGGAGCATCTCTGTGACCCCGCTGCCCTGTGAGAGAGCGACAGACACTCTCCGAGAT 679
DB 601 catctcctctctctgtgctgacgtcagctcgtctgtctctctctctctctccac 660
QY 680 CATCTCCTCTCTTCTTGTGGCGTGCAGCTGACGTGCTGTCTCTCTCCGCTCTCAC 739
DB 661 gctccgttctctgtgtttaaagcgaggcagaagaactcctgtatataatcaaacacc 720
QY 740 GCTCGTTCTCTGTGTAAACGGGGCAGAAAGAACTCCTGTATATATCAACAACAC 799
DB 721 attatgagaccagtaacaaactactcaagaagaatggtctgtagctccgattccaga 780
QY 800 ATTATGAGACCACTACAACTACTCAAGAGAGATGGCTGTAGCTGCCGATTTCCAGA 859
DB 781 agaagaagaagagatgtgaactgtgaatggaagtcataaggcgtgtggaactt 838
QY 860 AGAAGAAGAAGAGAGATGTGAACCTGTGAATGGAAGTCAATAGGGCTGTGGACTTT 917

RESULT 5
ID T39541 standard; cDNA to mRNA; 2347 BP.
AC T39541;
DT 12-DEC-1996 (first entry)
DE Mouse receptor 4-1BB cDNA.
KW Receptor 4-1BB; H4-1BB; monoclonal antibody; T-lymphocyte; T-cell;
KW Immunostimulant; cancer; autoimmune disease; graft rejection;
KW therapy; ss.
OS Mus sp.
FH Key Location/Qualifiers
FT CDS 146..916
FT /tag- a
FT mat_peptide 146..913
FT /tag- b
PN MO629348-A1.
PD 26-SEP-1996.
PF 22-MAR-1996; U03965.

Oy	472	AAGATGTTGCTCTTGGGACATTTAAACGATCAAGAAACGT---	GGCATCTGTGTGACCTTGGA	528
Db	555	cgaactgctctcttagaaggaagctcgtgctctaaagccggagacacgaagaagac	tg	614
Oy	529	CAAACTGTTCTTTTGGATGGAAAGTCGTGCTTTGGAATGGGACGAAGAGGACGTGG		588
Db	615	tgtgtgagacccctctgtgtgagctctctcc--agta--ccaccatctctgtgactcag		671
Oy	589	TCTGTGGACATCTCTACACCCGACCTCTCTCGGGAGCATCTCTGTGTGACCCCGCTGGCC		648
Db	672	agggaagacacgaagaggcaactcctctgcaggtcctaacctgttccctgtgcgtgcacatcg		731
Oy	649	CTGCAGAGAGACGAAGACACTCTCCGACAGATCATCTCTTCTTCTTGCGCTGACGTGGA		708
Db	732	cttgcctgcctcg--cc--ctgactctcaatcactctcctgttctctcgtgctcaaatgatca		788
Oy	709	CTGCGTTACTCTCTCTCGCTGTGTTCTTCCACAGCCCTCCGTTTCTCTGTGTAAACGGGGCA		768
Db	789	ggaaaaaattccccacatatatcaagcaacattagaagaagcaaccactcggagcagctcaag		848
	769	GAAGAAACCTCCTGTATATATTCAAACACACCACTTATAGACACAGTACAAACTCACTCAAG		828
Db	849	agggaagatgctctgtatgctgcgcgatgctccacaggaagaagaagaggga		895
Oy	829	AGGAAGATGGCTGTAGCTGCCGATTTCCAGAAGAAAGAAAGAGGAGA		875

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RESULT 7
ID 075428 standard; cDNA to mRNA; 768 BP.
AC 075428;
DT 08-AUG-1995 (first entry)
DE Murine 4-1BB polypeptide coding sequence.
KW T-cell; lymphocyte; activation; tissue culture; clone; cell lines;
KW proliferation; stimulation; 4-1BB-L; ligand; receptor; cytokine; ss.
OS Mus musculus.
FH key
FT CDS Location/Qualifiers
FT 1..768
FT /tag= a
FT /product= 4-1BB polypeptide.
FT sig_peptide 1..69
FT /tag= b
FT mat_peptide 70..768
FT /tag= c
FT WO9426290-A.
PN 24-NOV-1994.
PD 06-MAY-1994; U05036.
PE 07-MAY-1993; US-060843.
PR (IMM V ) IMMUNEX CORP.
DR Alderson MR, Goodwin RG, Smith CA;
DR WPI; 95-022265/03.
DR P-PSDB; R64199.
PT Cytokine; 4-1BB ligand (4-1BB-L) - binds to cell surface receptor
PT 4-1BB to transduce signal
PS Example 1, Page 43-44; 65pp; English.
CC The 4-1BB polypeptide (receptor) and the 4-1BB-L (cytokine, see
CC Q75422) are useful in a pharmaceutical composition for stimulating
CC the immune system. The 4-1BB and 4-1BB-L polypeptides are also useful
CC for exploring mechanisms of T-cell activation, as they are expressed
CC on T lymphocytes. 4-1BB-L can be used as a tissue culture reagent for
CC in vitro cultivation of primary T-cells during the derivation of
CC clonal T-cell lines. It may also be used to stimulate proliferation
CC of activated T-cells, used in therapeutic procedures.
CC Sequence 768 BP; 188 A; 186 C; 217 G; 177 T;

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Query Match	16.28;	Score 229;	DB 13;	Length 768;
Best Local Similarity	69.08;	Pred. No. 1.95e-115;		
Matches 524;	Conservative 0;	Mismatches 223;	Indels 12;	Gaps 8

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QY     120 ATGGGAACACGCTGTttACAACtTAGTAGCCACtCTGTtGCTGGTtCTCAACtTTGAGAG 179

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Db	61	gtggagacccgycagaaactcctctgataactcgtcaagctcgttaacttctcgc-aga-aat	118
Qy	180	ACAAATATATTGGAGGACTCTTTAGTAACTGCGCCAGCTGGTAACTTCTGTGATAATAAC	239
Db	119	acaatccag-ctcgaaagagctgcctcccaagtaactctctccagcataggtgagcagcg	177
Qy	240	AGGAATCAAGATTTCAGATGCCCTGTCTCTCCAAATATGTTTCTCCAGCGAGGTGGACAAAG	299
Db	178	aacttaacatctgcagagtgctgcagagctattccagttcaagaaagtttgcctct	237
Qy	300	ACCTGTGACATATGACAGCAGGTAAAGGTGTTTTCAGGACAGGAAGAGGTGTTCTCC	359
Db	238	accacaacgcgagagtgtagtgcaattgaagatccattgcttggggcaacagtgacc	29
Qy	360	ACCACCAATGCAGAGTGTGACTGCACCTCCAGGTTTCACTGCTCCGGGGGACAGATGCAGC	419
Db	298	agatgtgaagagactgtgaagcctcggccagagagctaaagcagcggttgcanaactgt	35
Qy	420	AGTGTGTGAACAGGATGTGAAACAAGTGAACAACTGACAAAAAAGGTTGTAAAGACTGT	479
Db	358	agcctggggaacaattaaatgaacagaaacgtaactcgtgcctctgcacctgaacgaactgc	417
Qy	480	TGCTTTGGGACTTTAAAGATCAGAAAGCT---GGCATCTGTCCACCTTGACCAAACTGT	536
Db	418	tctctagaacggaaggtctgtgcttaaagacccagcggaaccaaggaagaaacgtgtgtgcga	477
Qy	537	TCTTTGGATGGAAATCTGTGCTTGTGAATGGGACGAAGAGGAGACGTGTGTGTGGA	596
Db	478	ccccctgtgtgagctctctcc--agta-cacacattctgtgactccaagagagga	53
Qy	597	CCATCTCCAGCGACACTCTCTCCGGGAGACATCTGTGACCCCGCTGCCCTGCGAGA	656
Db	535	caagaaaggaacactcttcaaggtcttaacactgttcccgagcgcaatcgtccttctg	594
Qy	657	GAGCGAGGACATCTCCGCAATCATCTCTTCTTGTGGCTGAGAGTGACCTGCGCTTG	716
Db	595	ctgag-cc--ctgactctcatcactcctctgtctctctgtgcctcaatgatacgaagaaaa	651
Qy	717	CTCTTCTCTGCTTCTTCTCTCACGCTCCGTTTCTCTGTGTTAACGGCGCAGAAAGAA	776
Db	652	ttccccacataatcaagaaacattaaagaagacactgtagcagctcaagaggaaat	711
Qy	777	CTCTGTATATTTCAACAACACATTTATGAGCCAGTACAAACTACTCAAGAGAGAT	836
Db	712	gctgtagctgcagatgtccacaggaagaagaagagga	750
Qy	837	GGCTGTACTGCGGATTTCCGAAGAAATAAAGAGAGA	875

ID	035034	standard; DNA; 2649 BP.
AC	Q35034;	
DT	27-MAY-1993	(first entry)
DE	DNA fragment contg. ACE gene	intron 16.
KW	Angiotensin converting enzyme; polymorphism; detection; insertion;	
KW	vasoactive peptide metabolism; disease; hypertension; diagnosis;	
KW	atherosclerosis; granulomatous; sugar diabetes complications; ss.	
OS	Homio Septems.	
FH	Key	Location/Qualifiers
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FT /*tag- ad
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FT misc_feature 12952
FT /tag- ap
FT /note- "known polymorphic site"
FT misc_feature 13004
FT /tag- aq
FT /note- "known polymorphic site"
FT misc_feature 13009
FT /tag- ar
FT /note- "known polymorphic site"
FT misc_feature 13048
FT /tag- as
FT /note- "known polymorphic site"
FT misc_feature 13238
FT /tag- at
FT /note- "known polymorphic site"
FT misc_feature 13448
FT /tag- au
FT /note- "known polymorphic site"
FT misc_feature 13539
FT /tag- av
FT /note- "known polymorphic site"
FT misc_feature 13951
FT /tag- aw
FT /note- "known polymorphic site"
FT misc_feature 14041
FT /tag- ax
FT /note- "known polymorphic site"
FT misc_feature 14046
FT /tag- ay
FT /note- "known polymorphic site"
FT misc_feature 14475
FT /tag- az
FT /note- "known polymorphic site"
FT misc_feature 14874
FT /tag- ba
FT /note- "known polymorphic site"
FT misc_feature 14891
FT /tag- bb
FT /note- "known polymorphic site"
FT misc_feature 14966
FT /tag- bc
FT /note- "known polymorphic site"
FT intron 15024..15424
FT /tag- bd
FT /note- "intron 11"
FT misc_feature 15284
FT /tag- be
FT /note- "known polymorphic site"

FT exon 15425..15511
FT /tag- bf
FT /note- "exon 12"
FT intron 15512..15952
FT /tag- bg
FT /note- "intron 12"
FT misc_feature 15647..15659
FT /tag- bh
FT /note- "indefinite interval within intron 12"
FT exon 15953..16126
FT /tag- bi
FT /note- "exon 13"
FT misc_feature 16077
FT /tag- bj
FT /note- "known polymorphic site"
FT intron 16127..16565
FT /tag- bk
FT /note- "intron 13"
FT misc_feature 16243
FT /tag- bl

...
Note: remainder of annotations omitted.

Query Match 7.48; Score 105; DB 21; Length 24025;
Best Local Similarity 76.18; Pred. No. 1,93e+42;
Matches 175; Conservative 0; Mismatches 52; Indels 3; Gaps 3;

Db 7403 ggaattcaagaccagcctgccaacatgagagaaccctctacttaaaaaaaaaa 7462
||||| ||||||| ||||||| ||| ||||| ||| ||||| ||
CP 1286 GGAGTTGAGACCGCTGACACATGCGCAATGCACTTTACCAACAAAAACAA 1227
7463 aaaaattagccgggtggtgtgtatgctgtaattccagctactcaaggagctgagc 7522
||||| ||| ||||||| ||| ||||| ||| ||||| |||||
CP 1226 AAGAATTAGTCAGGTGCGTGCCCTCTTGATGTCAGCTACT AGAGACTGAGGC 1168
Db 7523 agagaatgcgttgaaac-ccaaggaagcagaaggttgcaagtgaagccaagatcgaccattgc 7581
||||| ||| ||||||| ||| ||| ||| ||||| ||||| |||
CP 1167 AGGAGATCATCTGAGCTCCAGAGTCAGGCTGCAGAGCCATGCTGTGCTGCCTGC 1108
Db 7582 actccagcctlagccaacaagaagtgaactcctcatcctcaaaaaaaaaa 7631
||||||| ||| ||| ||||| ||| ||| ||||| |||||
CP 1107 ACTCCAGCCTGGTGACCA-GAGTGAGACCTGTCAAAAAAAAAAAAAA 1059

RESULT 14
ID T17516 standard: cDNA: 24026 BP.
AC T17516;
DT 04-OCT-1996 (first entry)
DE Mutated BRCA1 genomic sequence from PM16.
KW Cancer therapy; breast and ovarian cancer predisposing gene; immunogen;
KW antibody production; germ-line alteration; probe; lesion neoplasia; human;
KW gene therapy; protein replacement therapy; protein mimetic; BRCA1; ds.
OS Homo sapiens.
FH Key Location/Qualifiers
FT exon 256..355
FT /tag- a
FT /note- "exon 1"
FT intron 356..1512
FT /tag- b
FT /note- "intron 1"
FT misc_feature 1295
FT /tag- c
FT /note- "known polymorphic site"
FT exon 1513..1611
FT /tag- d
FT /note- "exon 2"
FT intron 1612..2206
FT /tag- e
FT /note- "intron 2"
FT misc_feature 1925..1937
FT /tag- f
FT /note- "indefinite interval within intron 2"
FT misc_feature 2141

```
FT /tag- g
FT /note- "known polymorphic site"
FT exon 2207..2260
FT /tag- h
FT /note- "exon 3"
FT intron 2261..2677
FT /tag- i
FT /note- "intron 3"
FT misc.feature 2569..2581
FT /tag- j
FT /note- "indefinite interval within intron 3"
FT exon 2678..2788
FT /tag- k
FT /note- "exon 4"
FT misc.feature 2725
FT /tag- l
FT /note- "known polymorphic site"
FT intron 2789..3328
FT /tag- m
FT /note- "intron 4"
FT misc.feature 3063..3075
FT /tag- n
FT /note- "indefinite interval within intron 4"
FT exon 3329..3406
FT /tag- o
FT /note- "exon 5"
FT intron 3407..3813
FT /tag- p
FT /note- "intron 5"
FT misc.feature 3598..3610
FT /tag- q
FT /note- "indefinite interval within intron 5"
FT misc.feature 3653
FT /tag- r
FT /note- "known polymorphic site"
FT exon 3814..3902
FT /tag- s
FT /note- "exon 6"
FT intron 3903..4224
FT /tag- t
FT /note- "intron 6"
FT misc.feature 4076..4088
FT /tag- u
FT /note- "indefinite interval within intron 6"
FT exon 4225..4364
FT /tag- v
FT /note- "exon 7"
FT intron 4365..6571
FT /tag- w
FT /note- "intron 7"
FT misc.feature 4391..4392
FT /tag- x
FT /note- "known polymorphic site"
FT misc.feature 4602..4614
FT /tag- y
FT /note- "indefinite interval within intron 7"
FT misc.feature 6538
FT /tag- z
FT /note- "known polymorphic site"
FT exon 6572..6677
FT /tag- aa
FT /note- "exon 8"
FT intron 6678..9163
FT /tag- ab
FT /note- "intron 8"
FT misc.feature 6823
FT /tag- ac
FT /note- "known polymorphic site"
FT misc.feature 9106
FT /tag- ad
FT /note- "known polymorphic site"
FT exon 9164..9209
FT /tag- ae

FT /note- "exon 9"
FT misc.feature 9207
FT /tag- af
FT /note- "known polymorphic site"
FT intron 9210..10530
FT /tag- ag
FT /note- "intron 9"
FT misc.feature 9376
FT /tag- ah
FT /note- "known polymorphic site"
FT exon 10531..10607
FT /tag- ai
FT /note- "exon 10"
FT intron 10608..11597
FT /tag- aj
FT /note- "intron 10"
FT misc.feature 11384..11396
FT /tag- ak
FT /note- "indefinite interval within intron 10"
FT exon 11598..15023
FT /tag- al
FT /note- "exon 11"
FT misc.feature 11908
FT /tag- am
FT /note- "known polymorphic site"
FT misc.feature 11994
FT /tag- an
FT /note- "known polymorphic site"
FT misc.feature 12952
FT /tag- ao
FT /note- "known polymorphic site"
FT misc.feature 13004
FT /tag- ap
FT /note- "known polymorphic site"
FT misc.feature 13009
FT /tag- aq
FT /note- "known polymorphic site"
FT misc.feature 13048
FT /tag- ar
FT /note- "known polymorphic site"
FT misc.feature 13238
FT /tag- as
FT /note- "known polymorphic site"
FT misc.feature 13448
FT /tag- at
FT /note- "known polymorphic site"
FT misc.feature 13539
FT /tag- au
FT /note- "known polymorphic site"
FT misc.feature 13951
FT /tag- av
FT /note- "known polymorphic site"
FT misc.feature 14041
FT /tag- aw
FT /note- "known polymorphic site"
FT misc.feature 14046
FT /tag- ax
FT /note- "known polymorphic site"
FT misc.feature 14475
FT /tag- ay
FT /note- "known polymorphic site"
FT misc.feature 14874
FT /tag- az
FT /note- "known polymorphic site"
FT misc.feature 14891
FT /tag- ba
FT /note- "known polymorphic site"
FT misc.feature 14966
FT /tag- bb
FT /note- "known polymorphic site"
FT intron 15024..15424
FT /tag- bc
FT /note- "intron 11"
```



```

FT /note- "known polymorphic site"
FT misc_feature 9106
FT /tag- ad
FT /note- "known polymorphic site"
FT exon 9164..9209
FT /tag- ae
FT /note- "exon 9"
FT misc_feature 9207
FT /tag- af
FT /note- "known polymorphic site"
FT intron 9210..10530
FT /tag- ag
FT /note- "intron 9"
FT misc_feature 9376
FT /tag- ah
FT /note- "known polymorphic site"
FT exon 10531..10607
FT /tag- ai
FT /note- "exon 10"
FT intron 10608..11597
FT /tag- aj
FT /note- "intron 10"
FT misc_feature 11384..11396
FT /tag- ak
FT /note- "indefinite interval within intron 10"
FT exon 11598..15023
FT /tag- al
FT /note- "exon 11"
FT misc_feature 11908
FT /tag- am
FT /note- "known polymorphic site"
FT misc_feature 11994
FT /tag- an
FT /note- "known polymorphic site"
FT misc_feature 12952
FT /tag- ao
FT /note- "known polymorphic site"
FT misc_feature 13004
FT /tag- ap
FT /note- "known polymorphic site"
FT misc_feature 13009
FT /tag- aq
FT /note- "known polymorphic site"
FT misc_feature 13048
FT /tag- ar
FT /note- "known polymorphic site"
FT misc_feature 13238
FT /tag- as
FT /note- "known polymorphic site"
FT misc_feature 13448
FT /tag- at
FT /note- "known polymorphic site"
FT misc_feature 13539
FT /tag- au
FT /note- "known polymorphic site"
FT misc_feature 13951
FT /tag- av
FT /note- "known polymorphic site"
FT misc_feature 14041
FT /tag- aw
FT /note- "known polymorphic site"
FT misc_feature 14046
FT /tag- ax
FT /note- "known polymorphic site"
FT misc_feature 14475
FT /tag- ay
FT /note- "known polymorphic site"
FT misc_feature 14874
FT /tag- az
FT /note- "known polymorphic site"
FT misc_feature 14891
FT /tag- ba
FT /note- "known polymorphic site"

```

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FT misc_feature 14966
FT /tag- bb
FT /note- "known polymorphic site"
FT intron 15024..15424
FT /tag- bc
FT /note- "intron 11"
FT misc_feature 15284
FT /tag- bd
FT /note- "known polymorphic site"
FT exon 15425..15511
FT /tag- be
FT /note- "exon 12"
FT intron 15512..15952
FT /tag- bf
FT /note- "intron 12"
FT misc_feature 15647..15659
FT /tag- bg
FT /note- "indefinite interval within intron 12"
FT exon 15953..16126
FT /tag- bh
FT /note- "exon 13"
FT misc_feature 16077
FT /tag- bi
FT /note- "known polymorphic site"
FT intron 16127..16565
FT /tag- bj
FT /note- "intron 13"
FT misc_feature 16243
FT /tag- bk
FT /note- "known polymorphic site"
FT misc_feature 16370..16382
FT /tag- bl

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Note: remainder of annotations omitted.

Query Match 7.4%; Score 105; DB 21; Length 24026;
 Best Local Similarity 76.1%; Pred. No. 1,93e-42;
 Matches 175; Conservative 0; Mismatches 52; Indels 3; Gaps 3;

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Db 7404 ggaagtcagagcagcctgacacacatgagagaaaccccatctactaataaaaaa 7463
    ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Cp 1286 GGAATTGAGACGACGCTGTACAAACATGCGCAAAATGCCATCTTACCAACAAAAA 1227
    ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Db 7464 aaaaatagccggggtgtgtgtatgcctgtatccagctactcagaggtgagc 7523
    ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Cp 1226 AAAAGTTAGTCAGGTGTGTGCGCCCTTCTTGTAGTCCAGTACT-AGGAGACTGAGGC 1168
    ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Db 7524 agagaatcgctgaac-ccaggaagcagaggttgcagtgagccaagatgcaccattgc 7582
    ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Cp 1167 AGGAGGATCACTTGAGCTCCAGAGCTCAAGGCTGCAGAGAGCCATGCTGTCCTGCTGC 1108
    ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Db 7583 actccagcctaggcaacaagaagtgaacatccatctcaaaaaaaaaa 7632
    ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Cp 1107 ACTCCAGCCTGGTGACA-GAGTGAGACCTGTCAAAAAAAAAAAAAA 1059
    ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||

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Search completed: Wed Mar 25 13:32:37 1998
 Job time : 213 secs.


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Oy 61 TCDCIRCKGKGVTRKREKSGSTSNABEDCTGRPHCLGAGCSMCEQDCKQCKQLTKKGCXDC 120
Db 121 cftgtdndqkrgricrptwncslgkxvlyngtkerdyvegspadlspgassvtpapare 180
Oy 121 CFTGTNDQKRGICRPTWNCSLDGKSVLYNGTKERDYVEGSPADLSPGASSVTPAPARE 180
Db 181 pghsqjissfialstallflflltrfsvkrgrklllyfkqpfmrpqttgdeed 240
Oy 181 PEGHSQJISSFIALSTALLFLFLTRFSVVKRGRKLLYFKQPFMRPVQTTQDEED 240
Db 241 cscrfpeeeegcel 255
Oy 241 CSCRFPEEEEGGCEL 255

RESULT 2
ENTRY B32393 #type complete
TITLE T-cell antigen 4-1BB precursor - mouse
ORGANISM #formal_name Mus musculus #common_name house mouse
DATE 17-Jul-1992 #sequence_revision 17-Jul-1992 #text_change
02-Aug-1996
SESSIONS B32393; I48879
REFERENCE A32393
#authors Kwon, B.S.; Weissman, S.M.
#journal Proc. Natl. Acad. Sci. U.S.A. (1989) 86:1963-1967
#title cDNA sequence of two inducible T-cell genes.
#cross-references MUID:89184547
#accession B32393
#molecule_type mRNA
#residues 1-256 #label KWO
#cross-references GB:J04492
REFERENCE I48879
#authors Kwon, B.S.; Kozak, C.A.; Kim, K.K.; Pickard, R.T.
#journal J. Immunol. (1994) 152:2256-2262
#title Genomic Organization and Chromosomal Localization of the
T-cell Antigen 4-1BB.
#cross-references MUID:94179805
#accession I48879
#status preliminary; translated from GB/EMBL/DBJ
#molecule_type DNA
#residues 1-256 #label RES
#cross-references EMBL:U02567; NID:g409177; CDS_PID:g409178
GENETICS 35/1. 69/1; 115/1; 138/2; 156/3; 181/1; 225/1
CLASSIFICATION #superfamily NGF receptor repeat homology
KEYWORDS transmembrane protein
FEATURE 1-23
1-23 #domain signal sequence #status predicted #label SIG\
P4-256 #product 4-1BB protein #status predicted #label MAT
MAYR #length 256 #molecular-weight 27598 #checksum 4884

Query Match 58.0%; Score 1116; DB 16; Length 256;
Best Local Similarity 57.3%; Pred. No. 6,29e-164;
Matches 145; Conservative 49; Mismatches 55; Indels 4; Gaps 4;

Db 1 mgncynvnyvlllygcekvavqnsdcngpctfckry-npvksccpsfssfggqp 59
Oy 1 MGNCSYNYVATLLVLYNERTSLDDPCNCPAGTFCDDNNRQIISPCPPNFSFSSAGGR 60
Db 60 ncnlrvagyrffkfcstnaaceclcgfnclgpgctckdrppgltkgckc 119
Oy 61 TCDIRCKGKGVTRKREKSGSTSNABEDCTGRPHCLGAGCSMCEQDCKQCKQLTKKGCXDC 120
Db 120 slgtfndngtvtcrptwncslgkxvlyngtkerdyvegspadlspgassvtpapare 179
Oy 121 CFTGTNDQKRGICRPTWNCSLDGKSVLYNGTKERDYVEGSPADLSPGASSVTPAPAR 179
Db 180 g-ghslgyltflalts-allaiflcllsvlwrkfkphlktkqpfkktgaageed 237
Oy 180 EPGHSQJISSFIALSTALLFLFLTRFSVVKRGRKLLYFKQPFMRPVQTTQDEED 239
Db 238 acscrcpgeeg 250

```

```

Oy 240 GCSRFPEEEEGG 252

RESULT 3
ENTRY A49053 #type complete
TITLE CD27 antigen precursor - mouse
ALTERNATE_NAMES CD27L receptor; T cell activation antigen CD27
ORGANISM #formal_name Mus musculus #common_name house mouse
DATE 19-Dec-1993 #sequence_revision 22-Apr-1995 #text_change
22-Apr-1995
ACCESSIONS A49053
REFERENCE A49053
#authors Gravestein, L.A.; Blom, B.; Nolten, L.A.; de Vries, E.; van
der Horst, G.; Ossendrop, F.; Borst, J.; Loeenen, W.A.
#journal Eur. J. Immunol. (1993) 23:943-950
#title Cloning and expression of murine CD27: comparison with 4-1BB,
another lymphocyte-specific member of the nerve growth
factor receptor family.
#cross-references MUID:93209296
#accession A49053
#molecule_type mRNA
#residues 1-250 #label GRA
#cross-references NCBIN:128168; NCBIP:128169
CLASSIFICATION #sequence extracted from NCBIP backbone
KEYWORDS duplication; glycoprotein; homodimer; receptor; surface
antigen; T-cell; transmembrane protein
FEATURE 1-20
1-182 #domain signal sequence #status predicted #label SIG\
27-63 #domain extracellular #status predicted #label EXT\
65-105 #domain NGF receptor repeat homology #label NG1\
121-179 #region proline/serine/threonine-rich
183-202 #domain transmembrane #status predicted #label TMN\
203-250 #domain intracellular #status predicted #label INT\
95,182 #binding site carbohydrate (asn) (covalent) #status
predicted

SUMMARY #length 250 #molecular-weight 28164 #checksum 6216

Query Match 10.7%; Score 206; DB 2; Length 250;
Best Local Similarity 37.1%; Pred. No. 3,29e-14;
Matches 26; Conservative 14; Mismatches 26; Indels 4; Gaps 4;

Db 53 cegataaqcpcipgtsfspdnyhtrpescrcnsgflirn-ctvtanaescskwng 111
Oy 37 CDNNNMQI-CSPC-PNFSFSSAGGQRT-CDICRCKGKGVTRKREKSGSTSNABEDCTGRPH 93
Db 112 crdgectec 121
Oy 94 CLGAGCSMCE 103

RESULT 4
ENTRY A46517 #type complete
TITLE CD27 antigen precursor - human
ALTERNATE_NAMES CD27L receptor; T cell activation antigen CD27
ORGANISM #formal_name Homo sapiens #common_name man
DATE 18-Jun-1993 #sequence_revision 22-Apr-1995 #text_change
23-Feb-1997
ACCESSIONS A46517; A46454
REFERENCE A46517
#authors Loeenen, W.A.; Gravestein, L.A.; Beumer, S.; Melief, C.J.;
Hagemeljer, A.; Borst, J.
#journal J. Immunol. (1992) 149:3937-3943
#title Genomic organization and chromosomal localization of the
human CD27 gene.
#cross-references MUID:93094588
#accession A46517
#molecule_type DNA
#residues 1-260 #label IOE
#cross-references NCBIP:120386

```

```

#sequence extracted from NCBI backbone
#note authors propose an alternative repeat pattern
REFERENCE A46454
#authors Camerini, D.; Walz, G.; Loenen, W.A.; Borst, J.; Seed, B.
#journal J. Immunol. (1991) 147:3165-3169
#title The T cell activation antigen CD27 is a member of the nerve
#cross-references MIM:92013149 growth factor/tumor necrosis factor receptor gene family.
#accession A46454
##molecule-type mRNA
##residues 1-58, 'A', 60-260 #label CAM
##cross-references NCBI:60285; NCBI:60289
#note sequence extracted from NCBI backbone
COMMENT A soluble CD27 found in serum and urine is formed by proteolysis.
GENETICS
#gene GDB:CD27
##cross-references GDB:132582
#map_position 12p13-12p13
#introns 46/1; 90/1; 150/1; 180/1; 220/1
#STRUCTURE
#FUNCTION
#SIGNIFICATION
#SUPERFAMILY
#DOMAINS
#FEATURES
1-20 #domain signal sequence #status predicted #label SIG\
21-191 #domain extracellular #status predicted #label Ext\
27-63 #domain NGF receptor repeat homology #label NG1\
65-105 #domain NGF receptor repeat homology #label NG2\
121-188 #region proline/serine/threonine-rich\
192-211 #domain transmembrane #status predicted #label TMN\
212-260 #domain intracellular #status predicted #label INT\
95 #binding_site carbohydrate (Asn) (covalent) #status predicted
SUMMARY #length 260 #molecular-weight 29186 #checksum 1652
Query Match 10.3%; Score 198; DB 2; Length 260;
Best Local Similarity 38.6%; Pred. No. 4,52e-13;
Matches 27; Conservative 14; Mismatches 25; Indels 4; Gaps 4
Db 53 cdghrkacqpcipgvsfspdhttrhpcscrhnsqllvtn-clltanacacrnqwg 111
||:|:| | | | | | | | | | | | | | | | | | | | | | | | | |
QY 37 CDNNRNQI-CSPSPN-SFSSAGGRT-CDICRQCKGVFRTRKESSTSMACDCTPGH 93
||:|:| | | | | | | | | | | | | | | | | | | | | | | | | |
Db 112 crkxctecd 121
||:|:| | | | | | | | | | | | | | | | | | | | | | | | | |
QY 94 CIGAGCSMCE 103
||:|:| | | | | | | | | | | | | | | | | | | | | | | | | |
#CULT 5
#RT
#TITLE GQVZML #type complete
#ORGANISM T2 protein - myxoma virus (strain Lausanne)
#DATE 31-Dec-1992 #sequence_revision 31-Dec-1992 #text_change 26-Apr-1996
ACCESSIONS A40566
REFERENCE A40566
#authors Upton, C.; Macen, J.L.; Schreiber, M.; Mcfadden, G.
#journal Virology (1991) 184:370-382
#title Myxoma virus expresses a secreted protein with homology to the tumor necrosis factor receptor gene family that contributes to viral virulence.
#cross-references MIM:91335768
#accession A40566
##molecule-type DNA
##residues 1-326 #label UPT
##cross-references GB:M37976
CLASSIFICATION #superfamily myxoma virus T2 protein; NGF receptor repeat homology
KEYWORDS glycoprotein
FEATURE #domain NGF receptor repeat homology #label NG2\
64-105 #domain NGF receptor repeat homology #label NG3\
106-147 #binding_site carbohydrate (Asn) (covalent) #status predicted
66,181,205,238

```

```

SUMMARY #length 326 #molecular-weight 35208 #checksum 9255

Query Match          9.5%; Score 183; DB 2; Length 326;
Best Local Similarity 31.5%; Pred.No.5,72e-11;
Matches      28; Conservative    20; Mismatches   32; Indels     9; Gaps     5

D> ctscppgyasrllgpgsdvctspcknetffastnhabavcsrcrgtghssgsdkt 99
|::||::|: |::|::|::|::|::|::|: |: ||::|: |::|: |::|: |::|:
QY 28 CSNCPAGF----CDNNRNQJCSFCPPNSFSASGQ-RITDICR-QCKGVRTTRKESST 81

Db       100 rdrydcasaagnycllkqsgcriapkl 128
|::||::| |::|::|::|::|::|::|: |::|: |::|: |::|: |::|:
QY      82 SNAECDCTPGRHCL--G-AGCSCMEDPOCK 107


RESULT        6
ENTRY         S32385           #type fragment
TITLE         gene G4R protein - variola virus (fragment)
ORGANISM      #formal name Variola virus
DATE          19-Mar-1997 #sequence_revision 19-Mar-1997 #text_change
              19-Mar-1997

ACCESSIONS
REFERENCE
#authors      Shchelkunov, S.N.; Blinov, V.M.; Sandakhchiev, L.S.
#journal      FEBS Lett. (1993) 319:80-83
#title        Genes of variola and vaccinia viruses necessary to overcome
               the host protective mechanisms.
#accesion     S32385
#status       preliminary
#residues     1-138 ##label SHC
#cross-references EMBL:X69198
SUMMARY       #length 138 #checksum 6036

Query Match          9.3%; Score 179; DB 18; Length 138;
Best Local Similarity 34.1%; Pred.No.2,04e-10;
Matches      29; Conservative    20; Mismatches   29; Indels     7; Gaps     4

D> clscppgyasrlcdskntlgtctcgsgtlfsrmhlpaclscngcrnsqvetscnt 73
|::||::|: |::|::|::|::|::|::|: |: |::|: |::|: |::|: |::|:
QY 28 CSNCPAGF---CDNNRNQJCSFCPPNSFSASGQ-RITDICR-QCKGVRTTRKESST 81

D> hmlcecsygyallkgssgc-kac 97
|::||::|: |::|::|::|::|::|::|: |::|: |::|: |::|: |::|:
QY      82 SNAECDCTPGRHCLGAGCSMCEPDO 106


RESULT        7
ENTRY         D36858           #type complete
TITLE         G4R protein - variola virus
ALTERNATE_NAMES B28R protein (COP)
ORGANISM        #formal name Variola virus
DATE            30-Sep-1993 #sequence_revision 30-Sep-1993 #text_change
              31-Nov-1996

ACCESSIONS
REFERENCE
#authors      A36859
Blinov, V.M.
#submission   submitted to GenBank, November 1992
#description   not shown.
#accesion     D36858

#molecule_type DNA
#statucus     preliminary
#residues     1-349 ##label BLI
#cross-references GB:X69198
REFERENCE     S46868
#experimental source strain India-1967, ssp. major, isolate Ind3
AUTHORS      Kolykhvalov, A.A.; Blinov, V.M.; Gtorov, V.V.; Pozdnjakov,
              S.G.; Chizhikov, V.E.; Frolow, I.V.; Totmenin, A.V.;
              Shchelkunov, S.N.; Sandakhchiev, L.S.
#submission   Submitted to the EMBL Data Library, April 1992
#description   Nucleotide sequence analysis of the region of variola virus
XhoI F O H P Q genome fragment.
#accesion     S46868
#status       preliminary

```

```
##molecule_type DNA
##residues 1-349 ##label KOL
##cross-references EMBL:X67117
##experimental_source strain India-1967, isolate Ind3
CLASSIFICATION #superfamily NGF receptor repeat homology
FEATURE
68-109 #domain NGF receptor repeat homology #label NG2\
110-151 #domain NGF receptor repeat homology #label NG3
SUMMARY #length 349 #molecular-weight 38189 #checksum 2016

Query Match 9.3%; Score 179; DB 9; Length 349;
Best Local Similarity 34.1%; Pred. No. 2.04e-10;
Matches 29; Conservative 20; Mismatches 29; Indels 7; Gaps 4;

Db 44 clscppgyarldskntqctpgsgftsrnhlpclscngscnsgnvetrcntt 103
OY 28 CSNCPAGTIF---CDNNNQICSPCPNPFSSAGGQ-RTCDICR-QCKGVFRTREKCSST 81
| : : : : : | : : : : : | : : : : : | : : : : : | : : : : : |
Db 104 hnricecspgyyalkgssgc-kac 127
OY 82 SNABEDCTPFHCLGAGCSMCEQDC 106
| : : : : : | : : : : : | : : : : : | : : : : : | : : : : : |

RESULT 8
ENTRY B43692 #type complete
TITLE T2 protein - rabbit fibroma virus
ORGANISM #formal_name rabbit fibroma virus, Shope fibroma virus
DATE 30-Sep-1993 #sequence_revision 30-Sep-1993 #text_change 23-May-1997

ACCESSIONS B43692
REFERENCE A43692
#authors Upton, C.; Delange, A.M.; McFadden, G.
#journal Virology (1987) 160:20-30
#title Tumorigenic poxviruses: genomic organization and DNA sequence of the telomeric region of the Shope fibroma virus genome.

#accession B43692
#status preliminary
#molecule_type DNA
#residues 1-325 ##label UPT
#cross-references GB:M17433
CLASSIFICATION #superfamily myxoma virus T2 protein; NGF receptor repeat homology

FEATURE
64-105 #domain NGF receptor repeat homology #label NG2\
106-147 #domain NGF receptor repeat homology #label NG3
SUMMARY #length 325 #molecular-weight 35132 #checksum 4629

Query Match 9.0%; Score 174; DB 6; Length 325;
Best Local Similarity 31.3%; Pred. No. 9.91e-10;
Matches 25; Conservative 15; Mismatches 35; Indels 5; Gaps 4;

Db 49 asrlcpgpsntvcspcdgtftasthnapacvscrgpctghlscspcdtrhdyvncst 108
OY 33 AGTCDDNNRNQICSPCPNPFSSAGGQ-RTCDICR-QCKGVFRTREKCSSTNAECDDCTP 90
| : : : : : | : : : : : | : : : : : | : : : : : | : : : : : |
Db 109 gnycllkgngcricapqtk 128
OY 91 GFHCL--G-AGCSMCEQDC 107
| : : : : : | : : : : : | : : : : : | : : : : : | : : : : : |

RESULT 9
ENTRY A46515 #type complete
TITLE B cell-associated surface molecule CD40 - mouse
ORGANISM #formal_name Mus musculus #common_name house mouse
DATE 18-Jun-1993 #sequence_revision 18-Nov-1994 #text_change 03-Mar-1995

ACCESSIONS A46515
REFERENCE A46515
#authors Grimaldi, J.C.; Torres, R.; Kozak, C.A.; Chang, R.; Clark, E.A.; Howard, M.; Cockayne, D.A.
#journal J. Immunol. (1992) 149:3921-3926
#title Genomic structure and chromosomal mapping of the murine CD40 gene.
```

```
##cross-references MUID:93094586
#accession A46515
#status preliminary; not compared with conceptual translation
#molecule_type nucleic acid
#residues 1-289 ##label GRI
##cross-references NCBI:P120357
##experimental_source BALB/c, liver
#note sequence extracted from NCBI backbone
SUMMARY #length 289 #molecular-weight 32111 #checksum 579

Query Match 8.9%; Score 171; DB 16; Length 289;
Best Local Similarity 31.2%; Pred. No. 2.54e-09;
Matches 43; Conservative 21; Mismatches 58; Indels 16; Gaps 11;

Db 51 ctalekq-chnpdsgefsaqwrelnrhqhrhcepnqglrvkkgtaesdvctckegq 109
OY 37 CDN-NRNQICSPCPNPFSSA-GGQRTCDICRQCK-G-VRTTRKCSSTNAECDDCTPFG 92
| : : : : : | : : : : : | : : : : : | : : : : : | : : : : : |
Db 110 hctskdeacaghtpcipgfygmamatetdvtchpcpvyffnsgslfckypwtscd 169
OY 93 HCLGAGCSMCEQD--CKQG---DEL-T-KKG--CKDCCFGFNDQKR--GICRWNTCSL 141
| : : : : : | : : : : : | : : : : : | : : : : : | : : : : : |
Db 170 knlevlqgtsqtnvicg 187
OY 142 DGKSVLVNGTKERDVCYG 159
| : : : : : | : : : : : | : : : : : | : : : : : | : : : : : |

RESULT 10
ENTRY A46476 #type complete
TITLE CD40 - mouse
ORGANISM #formal_name Mus musculus #common_name house mouse
DATE 18-Jun-1993 #sequence_revision 18-Nov-1994 #text_change 16-Feb-1997

ACCESSIONS A46476
REFERENCE A46476
#authors Torres, R.M.; Clark, E.A.
#journal J. Immunol. (1992) 148:620-626
#title Differential increase of an alternatively polyadenylated mRNA species of murine CD40 upon B lymphocyte activation.

#cross-references MUID:92105763
#accession A46476
#status preliminary
#molecule_type mRNA
#residues 1-305 ##label TOR
##cross-references NCBIN:75206; NCBI:P:75207
#note sequence extracted from NCBI backbone
KEYWORDS transmembrane protein
SUMMARY #length 305 #molecular-weight 33617 #checksum 5203

Query Match 8.9%; Score 171; DB 16; Length 305;
Best Local Similarity 31.2%; Pred. No. 2.54e-09;
Matches 43; Conservative 21; Mismatches 58; Indels 16; Gaps 11;

Db 51 ctalekq-chnpdsgefsaqwrelnrhqhrhcepnqglrvkkgtaesdvctckegq 109
OY 37 CDN-NRNQICSPCPNPFSSA-GGQRTCDICRQCK-G-VRTTRKCSSTNAECDDCTPFG 92
| : : : : : | : : : : : | : : : : : | : : : : : | : : : : : |
Db 110 hctskdeacaghtpcipgfygmamatetdvtchpcpvyffnsgslfckypwtscd 169
OY 93 HCLGAGCSMCEQD--CKQG---DEL-T-KKG--CKDCCFGFNDQKR--GICRWNTCSL 141
| : : : : : | : : : : : | : : : : : | : : : : : | : : : : : |
Db 170 knlevlqgtsqtnvicg 187
OY 142 DGKSVLVNGTKERDVCYG 159
| : : : : : | : : : : : | : : : : : | : : : : : | : : : : : |

RESULT 11
ENTRY S12783 #type complete
TITLE OX40 antigen precursor - rat
ALTERNATE_NAMES nerve growth factor receptor homolog
ORGANISM #formal_name Rattus norvegicus #common_name Norway rat
DATE 30-Sep-1993 #sequence_revision 30-Sep-1993 #text_change 30-May-1997
```

```

ACCESSIONS      S12783; S08036
REFERENCE        S12783
#authors        Mallett, S.; Fossum, S.; Barclay, A.N.
#journal         EMBO J. (1990) 9:1063-1068
#title           Characterization of the MRC OX40 antigen of activated CD4
                 positive T lymphocytes - a molecule related to nerve growth
                 factor receptor.
#cross-references MIMD:90214614
#accession       S12783
#molecule_type mRNA
#residues        1-271 ##label MAL
##cross-references EMBL:X17037
KEYWORDS         growth factor receptor; transmembrane protein
FEATURE         1-19
                20-271 #domain signal sequence #status predicted #label SIG\
                211-235 #product OX40 antigen #status predicted #label MAR\
                211-235 #domain transmembrane #status predicted #label TMM
SUMMARY          #length 271 #molecular-weight 29895 #checksum 379

Query Match      8.6%; Score 166; DB 16; Length 271;
Best Local Similarity 30.6%; Pred. No. 1.21e-08;
Matches 38; Conservative 25; Mismatches 48; Indels 13; Gaps 5;

Db 51 cdhrdvchpccgfyfneavydtkgcqchrsagslknctptdvtvcgcpqrg- 109
OY 37 CDNRNNOICSPCPNPSSSAGGORTCDICQCC--KGVFRTKREKSTSNABEDCTPGRHC 94
Db 110 -----pr--shk1gv-dcvpppphfpspgnackpwtncletslgqrlrhpasnl 159
OY 95 LGAGCSMCEDDCKRGQGLTRKGGCKDCDFGRFNNQKRGICRPWTNCSLDCKSVLVNGTHER 154
Db 160 dtvc 163
OY 155 DYVC 158

RESULT 12
ENTRY          I54182 #type complete
TITLE          tumor necrosis factor receptor 2-related protein - human
ORGANISM       Homo sapiens #common_name man
DATE           24-May-1996 #sequence_revision 24-May-1996 #text_change
               11-Apr-1997
ACCESSIONS     I54182
REFERENCE      I54182
#authors       Baens, M.; Chaffanet, M.; Cassiman, J.J.; Van den Berghe, H.;
               Marynen, P.
#journal       Genomics (1993) 16:214-218
#title         Construction and evaluation of a hncDNA library of human 12p
               transcribed sequences derived from a somatic cell hybrid.
#cross-references MIMD:93252381
#accession     I54182
#status        preliminary; translated from GB/EMBL/DBJ
#molecule_type mRNA
#residues      1-435 ##label RES
#cross-references GB:L04270; NID:g9339761; CDS_PID:g9339762
GENETICS       GDB:ITBR
#gene          GDB:ITBR
#cross-references GDB:1230195
SUMMARY        #length 435 #molecular-weight 46709 #checksum 63

Query Match      8.2%; Score 158; DB 16; Length 435;
Best Local Similarity 31.5%; Pred. No. 1.42e-07;
Matches 52; Conservative 26; Mismatches 66; Indels 21; Gaps 13;

Db 59 csrppgtysaksrirdvcatcaensynehmylttclqlcrpcdpymgjeiapcts 118
OY 28 CSNCPAGTF---CDNRNNOICSPCPNPSSSAGGORTCDICRCKGKGV--FRTREKSS 80
Db 119 krtgcgcqcmfcaaalctclhellcdpgpteelldxvgykgnhvpckaghtqnt 178
OY 81 TSNABCDCTPGRHGLG-A-GCSMCE--QDCKQG-Q-ELTR--KGGKDC--C-FGRF--ND 127
Db 179 ssparcphtrcengqlveaapgtadsttkcnpljppemsg 223

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RESULT	13
ENTRY	I48700
TITLE	gene ox40 protein - mouse
ALTERNATE_NAMES	Ox40 antigen
ORGANISM	formal name Mus musculus #common_name house mouse
DATE	02-Jul-1996 #sequence_revision 02-Jul-1996 #text_change 18-Oct-1996
ACCESSIONS	I48700; I48334; S34377
REFERENCE	I48700
authors	Calderhead, D.M.; Buhlmann, J.E.; van den Hertwegh, A.J.; Claassen, E.; Noelle, R.J.; Fell, H.P.
#journal	J. Immunol. (1993) 151:5261-5271
#title	Cloning of mouse Ox40: a T cell activation marker that may mediate T-B cell interactions.
#cross-references	MUID:94044750
#accession	I48700
#status	translated from GB/EMBL/DBJ
#molecule_type	mRNA
#residues	1-272 ##label RES
#cross-references	EMBL:221674; NID:g312827; CDS_PID:g312828
REFERENCE	I48334
authors	Birchland, M.L.; Copeland, N.G.; Gilbert, D.J.; Jenkins, N.A.; Barclay, A.N.
#journal	Eur. J. Immunol. (1995) 25:926-930
#title	Gene structure and chromosomal localization of the mouse homologue of rat Ox40 protein.
#cross-references	MUID:95255413
#accession	I48334
#status	translated from GB/EMBL/DBJ
#molecule_type	DNA
#residues	1-14,'G',16-272 ##label RB2
#cross-references	EMBL:X85214; NID:g732818; CDS_PID:g732819
GENETICS	
#gene	ox40
#introns	45/1; 86/1; 122/1; 144/2; 210/1; 250/1
SUMMARY	#length 272 #molecular_weight 30153 #checksum 841
Query Match	7.3%: Score 140; DB 16; Length 272;
Best Local Similarity	30.6%: Pred.No.3.08e-05;
Matches	36; Conservative 21; Mismatches 52; Indels 13; Gaps 5
Db	52 cdhtdrlchpoeitfyneavydtkqctcnhssgelskqncftqtdtvcrcrptq- 110
Oy	37 CDNNNQICSPCPPIPSFSAGGQRFCDICRQC--KGVETRTKECSSTINAECDCTPFPHC 94
Db	111 -----pr---gkykgyv-dcvppcpghfsppangackpwtncitssgkqtrhpasdl 160
Oy	95 LGAGCSMGEODCKQQLTLTKGCKKCCGFTNDQKRGICRPMTNCSLDGKSVLVNGTKER 154
Db	161 davec 164
Oy	155 DVVC 158
RESULT	14
ENTRY	A26431
TITLE	nerve growth factor receptor precursor, low affinity - rat
ALTERNATE_NAMES	NGF receptor
ORGANISM	formal name Rattus norvegicus #common_name Norway rat
DATE	19-Nov-1988 #sequence_revision 19-Nov-1988 #text_change 05-Apr-1995
ACCESSIONS	A26431; PH1229
REFERENCE	A26431
authors	Radeke, M.J.; Misko, T.P.; Hsu, C.; Herzenberg, L.A.; Shooter, E.M.
#journal	Nature (1987) 325:593-597
#title	Gene transfer and molecular cloning of the rat nerve growth factor receptor.
#cross-references	MUID:87115859

```

#accession      504460
##molecule_type      mRNA
##residues      1-277 ##label      STA
##cross-references      EMBL:X60592
REFERENCE
#authors      Braesch-Andersen, S.; Paulie, S.; Koho, H.; Nika, H.;
      Aspenstroem, P.; Perlmann, P.
#journal      J. Immunol. (1989) 142:562-567
#title      Biochemical characteristics and partial amino acid sequence
      of the receptor-like human B cell and carcinoma antigen
      CDw40.
#accession      A60771
##molecule_type      protein
##residues      21-50 ##label      BRA
##experimental_source      Burkitt lymphoma cell line Raji
GENETICS
#gene      GDB:CD40
##cross-references      GDB:215268
#map_position      20q12-20q13.2
KEYWORDS      B-cell; glycoprotein; phosphoprotein; surface antigen;
      transmembrane protein
FEATURE
1-20      #domain signal sequence #status predicted #label SIG\
21-277      #product B-cell activation protein CD40 #status
      experimental #label MAP\
21-193      #domain extracellular #status predicted #label EXT\
194-215      #domain transmembrane #status predicted #label TM\
216-277      #domain intracellular #status predicted #label CYT\
153,180      #binding_site carbohydrate (Asn) (covalent) #status
      predicted
SUMMARY      #length 277 #molecular_weight 30619 #checksum 6261
Query Match      7.1%, Score 136, DB 15, Length 277;
Best Local Similarity 28.3%; Pred. No. 9,83e-05;
Matches 39; Conservative 24; Mismatches 61; Indels 14; Gaps 10;
Db 51 cteftecclcgsgsefidwrmethqghydcpnjdlrvqgkgtsetdlticceagwh 110
QY 37 CDNNRNQICSPCPNPSSSAGGQRT-CDICRCK-GY-FRTKRCSTSNAECCCTPFGH 93
111 ctseacescvlhrgscpgfygkvqiatvsgdlcepcpvgffsnvsafechpvtscetk 170
QY 94 CLGAGCSNCE-Q-DCKGGQDELTK--KCKKD--C--C-FGTFNDCKRRI--CRPTNCSLD 142
Db 171 dlrvvgagatnktadvcp 188
QY 143 GKSYLVNQTKERDYVCGP 160

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MPSrch_DP protein - protein database search, using Smith-Waterman algorithm
Date: Tue Mar 24 17:03:43 1998; MasPar time 7.28 Seconds
Similar output not generated. 742.674 Million cell updates/sec

Title: >US-08-236-918A-8
Description: (1-253) From 5674704.pep
Perfect Score: 1925
Sequence: 1 MGNSCYNIVATLLVLNFER.....QEEGDCSCRFPEEEGCGCEL 255

Scoring table: PAM 150
Gap 11

Searched: 59021 seqs, 21210388 residues

Post-processing: Minimum Match 0%
Listing first 45 summaries

Database: swiss-prot34
1:part1 2:part2 3:part3 4:part4 5:part5 6:part6 7:part7
8:part8 9:part9 10:part10 11:part11

Statistics: Mean 45.059; Variance 89.948; scale 0.501

Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

Rank	Score	Query Match	Length	DB	ID	Description	Pred. No.
1	1925	100.0	255	1	41BB_HUMAN	4-1BB LIGAND RECEPTOR	0.00e+00
2	1116	58.0	256	1	41BB_MOUSE	4-1BB LIGAND RECEPTOR	6.16e-200
3	206	10.7	250	2	CD27_MOUSE	CD27L RECEPTOR PRECUR	1.05e-17
4	199	10.3	260	2	CD27_HUMAN	CD27L RECEPTOR PRECUR	1.67e-16
5	183	9.5	326	10	VT2_MXVL	TUMOR NECROSIS FACTOR	8.48e-14
6	183	9.5	415	9	TNRC_MOUSE	LYMPHOTOXIN-BETA RECE	8.48e-14
7	179	9.3	349	10	VC22_VAVR	PROTEIN C22/B28 HOMOL	3.93e-13
8	174	9.0	325	10	VT2_STVKA	TUMOR NECROSIS FACTOR	2.63e-12
9	171	8.9	289	2	CD40_MOUSE	CD40L RECEPTOR PRECUR	8.18e-12
10	166	8.6	271	7	OX40_RAT	OX40L RECEPTOR PRECUR	5.33e-11
11	158	8.2	435	9	TNRC_HUMAN	LYMPHOTOXIN-BETA RECE	1.03e-09
12	140	7.3	272	7	OX40_MOUSE	OX40L RECEPTOR PRECUR	6.53e-07
13	141	7.3	277	7	OX40_HUMAN	OX40L RECEPTOR PRECUR	4.60e-07
14	138	7.2	425	6	NGFR_RAT	LOW-AFFINITY NERVE GR	1.31e-06
15	136	7.1	277	2	CD40_HUMAN	CD40L RECEPTOR PRECUR	2.63e-06
16	135	7.0	427	6	NGFR_HUMAN	LOW-AFFINITY NERVE GR	3.71e-06
17	133	6.9	461	9	TNFR2_HUMAN	TUMOR NECROSIS FACTOR	7.37e-06
18	127	6.6	986	3	EPH3_HUMAN	TYROSINE-PROTEIN KINA	5.62e-05
19	127	6.6	993	3	EPH3_MOUSE	TYROSINE-PROTEIN KINA	5.62e-05
20	123	6.4	1609	6	LMG1_HUMAN	LAMININ GAMMA-1 CHAIN	2.12e-04
21	121	6.3	335	3	FASA_HUMAN	FAST RECEPTOR PRECURS	2.95e-04
22	121	6.3	474	9	TNFR2_MOUSE	TUMOR NECROSIS FACTOR	4.09e-04

Rank	Score	Query Match	Length	DB	ID	Description	Pred. No.
23	121	6.3	1607	6	LMG1_MOUSE	LAMININ GAMMA-1 CHAIN	4.09e-04
24	119	6.2	416	6	NGFR_CHICK	LOW-AFFINITY NERVE GR	7.84e-04
25	120	6.2	577	9	TRBM_MOUSE	THROMBOMODULIN PRECUR	5.67e-04
26	120	6.2	984	3	EPH2_HUMAN	TYROSINE-PROTEIN KINA	5.67e-04
27	119	6.2	1788	6	LMB1_DROME	LAMININ BETA-1 CHAIN	7.84e-04
28	117	6.1	713	6	TS4A_GIALA	MAJOR SURFACE-LABELLED	1.50e-03
29	118	6.1	755	2	COMP_RAT	CARTRIDGE OLIGOMERIC	1.08e-03
30	118	6.1	984	3	EPH2_RAT	TYROSINE-PROTEIN KINA	1.08e-03
31	117	6.1	1680	4	FUR2_DROME	FURIN-LIKE PROTEASE 2	1.50e-03
32	117	6.1	1786	6	LMB1_HUMAN	LAMININ BETA-1 CHAIN	1.50e-03
33	115	6.0	987	5	HTK_MOUSE	TYROSINE-PROTEIN KINA	2.83e-03
34	115	6.0	995	3	EPH3_CHICK	TYROSINE-PROTEIN KINA	2.83e-03
35	113	5.9	327	3	FASA_MOUSE	FAST RECEPTOR PRECURS	5.34e-03
36	113	5.9	461	9	TNFR1_RAT	TUMOR NECROSIS FACTOR	5.34e-03
37	114	5.9	1005	5	HTK_HUMAN	TYROSINE-PROTEIN KINA	3.89e-03
38	114	5.9	1005	5	EHK1_RAT	TYROSINE-PROTEIN KINA	3.89e-03
39	114	5.9	1712	9	TGFR_RAT	LATENT TRANSFORMING G	3.89e-03
40	112	5.8	454	9	TNFR1_MOUSE	TUMOR NECROSIS FACTOR	7.31e-03
41	108	5.6	1039	1	ATHL_HUMAN	POTASSIUM-TRANSPORTIN	2.53e-02
42	107	5.6	1786	6	LMB1_MOUSE	LAMININ BETA-1 CHAIN	3.43e-02
43	107	5.6	1801	6	LMB2_RAT	LAMININ BETA-2 CHAIN	3.43e-02
44	106	5.5	595	2	CD30L_HUMAN	CD30L RECEPTOR PRECUR	4.65e-02
45	106	5.5	915	7	PAC6_RAT	SERINE PROTEINASE PC6 P	4.65e-02

ALIGNMENTS

RESULT	ID	41BB_HUMAN	STANDARD	PRT	255 AA.
AC	Q07011	01-FEB-1995 (REL. 31, CREATED)			
DT	01-FEB-1995 (REL. 31, LAST SEQUENCE UPDATE)				
DT	01-FEB-1996 (REL. 33, LAST ANNOTATION UPDATE)				
DE	4-1BB LIGAND RECEPTOR PRECURSOR (T-CELL ANTIGEN 4-1BB HOMOLOG)				
DE	(T-CELL ANTIGEN IIA).				
GN	IIA.				
OS	HOMO SAPIENS (HUMAN).				
OC	EUCARYOTA; METAZOA; CHORDATA; VERTEBRATA; MAMMALIA;				
OC	EUTHERIA; PRIMATES.				
RN	[1]				
RP	SEQUENCE FROM N.A.				
RC	TISSUE-BLOOD;				
RX	MEDLINE; 94374434.				
RA	ALDERSON M.R., SMITH C.A., TOUGH T.W., DAVIS-SMITH T., ARMITAGE R.J.,				
RA	FAIK B., ROUX E., BAKER E., SUTHERLAND G.R., DIN W.S., GOODWIN R.G.,				
RL	EUR. J. IMMUNOL. 24:2219-2227(1994).				
RN	[2]				
RP	SEQUENCE FROM N.A.				
RC	TISSUE-BLOOD;				
RX	MEDLINE; 94085794.				
RA	SCHWARTZ H., TUCKERELL J., LOTZ M.;				
RA	GENE 134:295-298(1993).				
CC	-I- FUNCTION: RECEPTOR FOR THE PUTATIVE CYTOKINE 4-1BBL. POSSIBLY				
CC	ACTIVE DURING T CELL ACTIVATION.				
CC	-I- SUBCELLULAR LOCATION: TYPE I MEMBRANE PROTEIN.				
CC	-I- TISSUE SPECIFICITY: EXPRESSED ON THE SURFACE OF ACTIVATED T				
CC	CELLS.				
CC	-I- SIMILARITY: CONTAINS A LA-NGFR/TNFR-TYPE CYSTEINE-RICH REGION.				
DR	EMBL; U03197; G571321; -.				
DR	EMBL; L12964; G292238; -.				
DR	PROSITE; PS00652; TNFR_NGFR.				
KW	RECEPTOR; GLYCOPROTEIN; REPEAT; SIGNAL; TRANSMEMBRANE.				
FT	SIGNAL	1	17	POTENTIAL.	
FT	CHAIN	18	255	4-1BB LIGAND RECEPTOR.	
FT	DOMAIN	18	186	EXTRACELLULAR (POTENTIAL).	
FT	TRANSMEM	187	213	POTENTIAL.	
FT	DOMAIN	214	255	CYTOPLASMIC (POTENTIAL).	
FT	DOMAIN	47	159	3 X TNFR-CYS.	
FT	REPEAT	47	86	TNFR-CYS 1.	
FT	REPEAT	87	118	TNFR-CYS 2.	
FT	REPEAT	119	159	TNFR-CYS 3.	
FT	CARBOHYD	138	138	POTENTIAL.	
FT	CARBOHYD	149	149	POTENTIAL.	

```

FT CONFLICT 107 107 K -> R (IN REF. 2).
SQ SEQUENCE 255 AA; 27899 MW; 331C1176 CRC32;
Query Match 100.0%; Score 1925; DB 1; Length 255;
Best Local Similarity 100.0%; Pred. No. 0.00e+00;
Matches 255; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Db 1 mgnscynivaatl1llvnefrtslodpcsnpcagfcdnnnqicspcpnfsfssagqr 60
QY 1 MGNSCYNIVATLLVNEFRTRSLDPCSNCPAGTFCDDNNNQICSPCPNFSFSSAGQR 60
Db 61 tcdicrckgkyfrtrkesstsnacdcptgfhclgaagcsmcgedckgqdeltkgckdc 120
QY 61 TCDICRCKGKYFRTRKESSTSNACDCPTGFHCLGAGCSMCEDCKGQDELTKGCKDC 120
Db 121 cfcgfnndrk-gicrprwtncslldgksvlyngtkerdyvcgspadlspgassvtpapapare 180
QY 121 CFCGFNDRK-GICRPRWTNCSLDGKSVLYNGTKERDYVCGSPADLSPGASSVTPAPAPARE 180
Db 181 pghspqilseffaltstallflfllfrfsyvkrgkkllyfkrpmpvqtqeedg 240
QY 181 PGHSPQILSEFFALTSTALLFLFLLFRFSYVKRKKLLYFKRPMVPVQTQEEEDG 240
Db 241 cscrfpeeeeggccl 255
QY 241 CSCRFPEEEEGGCEL 255

RESULT 2
ID 41BB-MOUSE STANDARD; PRT; 256 AA.
AC P20334;
DT 01-FEB-1991 (REL. 17, LAST SEQUENCE UPDATE)
DT 01-FEB-1991 (REL. 17, LAST SEQUENCE UPDATE)
DE 01-FEB-1996 (REL. 33, LAST ANNOTATION UPDATE)
DE 4-1BB LIGAND RECEPTOR PRECURSOR (T-CELL ANTIGEN 4-1BB).
OS MUS MUSCULUS (MOUSE).
OC EUKARYOTA; METAZOA; CHORDATA; VERTEBRATA; TETRAPODA; MAMMALIA;
OC EUTHERIA; RODENTIA.
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE; 89184547.
RA KNON B.S.; WEISSMAN S.M.;
RA PROC. NATL. ACAD. SCI. U.S.A. 86:1963-1967(1989).
RN [2]
RP SEQUENCE FROM N.A.
RX STRAIN-BAB/C;
RX MEDLINE; 94179805.
RA KNON B.S.; KOZAK C.A.; KIM K.K.; PICKARD R.T.;
RA J. IMMUNOL. 152:2256-2262(1994).
RN [3]
RA CHARACTERIZATION, AND SEQUENCE OF 25-29.
RX MEDLINE; 9319510.
RA POLLOK K.E.; KIM Y.-J.; ZHOU Z.; HURTADO J.; KIN K.K.; PICKARD R.T.;
RA KNON B.S.;
RA J. IMMUNOL. 150:771-781(1993).
RN [4]
RP FUNCTION: RECEPTOR FOR THE PUTATIVE CYTOKINE 4-1BBL. POSSIBLY
ACTIVE DURING T CELL ACTIVATION.
CC -1- SUBUNIT: PRINCIPALLY AN HOMODIMER, BUT ALSO FOUND AS A MONOMER.
CC -1- SUBUNIT: ASSOCIATES WITH P56-LCK.
CC -1- INDUCTION: OPTIMAL BY PMA AND IONOMYCIN.
CC -1- TISSUE SPECIFICITY: EXPRESSED ON THE SURFACE OF ACTIVATED T-CELLS.
CC -1- SUBCELLULAR LOCATION: TYPE I MEMBRANE PROTEIN.
CC -1- SIMILARITY: CONTAINS A LA-NGFR/TNFR-TYPE CYSTEINE-RICH REGION.
DR EMBL; J04492; G401122; -.
DR EMBL; U02567; G409178; -.
DR PIR; B32393; B32393.
DR PROSITE; PS00652; TNFR_NGFR.
KW RECEPTOR; GLYCOPROTEIN; REPEAT; SIGNAL; TRANSMEMBRANE.
FT SIGNAL 1 24
FT CHAIN 25 256 4-1BB LIGAND RECEPTOR.
FT DOMAIN 25 187 EXTRACELLULAR (POTENTIAL).
FT TRANSEM 188 208 POTENTIAL.
FT DOMAIN 209 256 CYTOPLASMIC (POTENTIAL).

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FT DOMAIN 17 159 4 X TNFR-CYS.
FT REPEAT 17 45
FT REPEAT 46 85 TNFR-CYS 1.
FT REPEAT 86 117 TNFR-CYS 2.
FT REPEAT 118 159 TNFR-CYS 3.
FT REPEAT 128 159 TNFR-CYS 4.
FT CARBOHYD 128 128 POTENTIAL.
FT CARBOHYD 138 138 POTENTIAL.
SQ SEQUENCE 256 AA; 27598 MW; 5C2352FC CRC32;
Query Match 58.0%; Score 1116; DB 1; Length 256;
Best Local Similarity 57.3%; Pred. No. 6.16e-200;
Matches 145; Conservative 49; Mismatches 55; Indels 4; Gaps 4;

Db 1 mgnscynivaatl1llvnefrtslodpcsnpcagfcdnnnqicspcpnfsfssagqr 59
QY 1 MGNSCYNIVATLLVNEFRTRSLDPCSNCPAGTFCDDNNNQICSPCPNFSFSSAGQR 60
Db 60 ncnlcrvaagfyfrfkfsshaeccciegfhclgpaqctcekdcrpgqeltkgcktc 119
QY 61 TCDICRCKGKYFRTRKESSTSNACDCPTGFHCLGAGCSMCEDCKGQDELTKGCKDC 120
Db 120 slgftndqngtgvcrpwtncslldgksvlyngtkerdyvcgspadlspgassvtpapapare 179
QY 121 CFCGFNDRK-GICRPRWTNCSLDGKSVLYNGTKERDYVCGSPADLSPGASSVTPAPAPARE 179
Db 180 g-gphsqyltflalts-allatllflfsvlykwrkkrphfkqpfkttgaageed 237
QY 180 PGHSPQILSEFFALTSTALLFLFLLFRFSYVKRKKLLYFKRPMVPVQTQEEED 239
Db 238 acscrfpeeeeggccl 250
QY 240 GCSCRFPEEEEGGCEL 252

RESULT 3
ID CD27-MOUSE STANDARD; PRT; 250 AA.
AC P41272;
DT 01-FEB-1995 (REL. 31, LAST SEQUENCE UPDATE)
DT 01-FEB-1995 (REL. 31, LAST SEQUENCE UPDATE)
DE 01-FEB-1995 (REL. 31, LAST ANNOTATION UPDATE)
DE CD27L RECEPTOR PRECURSOR (T-CELL ACTIVATION ANTIGEN CD27).
GN CD27.
OS MUS MUSCULUS (MOUSE).
OC EUKARYOTA; METAZOA; CHORDATA; VERTEBRATA; TETRAPODA; MAMMALIA;
OC EUTHERIA; RODENTIA.
RN [1]
RP SEQUENCE FROM N.A.
RX STRAIN-B6/CBAF1; TISSUE-THYMUS;
RX MEDLINE; 93209286.
RA GRAVESTON L.A.; BLOM B.; NOJEN L.A.; DE VRIES E.; VAN DER HORST G.;
RA OSSENDORP F.; BORST J.; LOENEN W.A.;
RA EUR. J. IMMUNOL. 23:943-950(1993).
RN [2]
RP FUNCTION: RECEPTOR FOR A CYTOKINE LIGAND KNOWN AS CD27L. MAY PLAY
A ROLE IN SURVIVAL OF ACTIVATED T-CELLS.
CC -1- SUBUNIT: HOMODIMER (BY SIMILARITY).
CC -1- SUBCELLULAR LOCATION: TYPE I MEMBRANE PROTEIN.
CC -1- TISSUE SPECIFICITY: IN THYMUS AND SPLEEN, BUT NOT IN NON-LYMPHOID
TISSUES.
CC -1- SIMILARITY: CONTAINS A LA-NGFR/TNFR-TYPE CYSTEINE-RICH REGION.
DR EMBL; L24495; -. NOT_ANNOTATED_CDS.
DR PIR; A49053; A49053.
DR PROSITE; PS00652; TNFR_NGFR.
KW T-CELL; GLYCOPROTEIN; TRANSMEMBRANE; SIGNAL; RECEPTOR; REPEAT.
FT SIGNAL 1 20
FT CHAIN 21 250 CD27L RECEPTOR.
FT DOMAIN 21 182 EXTRACELLULAR (POTENTIAL).
FT TRANSEM 183 203 POTENTIAL.
FT DOMAIN 204 250 CYTOPLASMIC (POTENTIAL).
FT DOMAIN 204 250 3 X TNFR-CYS.
FT REPEAT 26 141 TNFR-CYS 1.
FT REPEAT 64 104 TNFR-CYS 2.
FT REPEAT 105 141 TNFR-CYS 3.
FT CARBOHYD 95 95 POTENTIAL.

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RA FORCE MR., WILLIAMS-ABBOTT L., BRONNING J., HESSION C., TIZARD R.,  
RL MAER C.F.: TO EMBL/GENBANK/DDBJ DATA BANKS.  
RN [2]  
RP SEQUENCE FROM N.A.  
RX MEDLINE; 9616385.  
RA MAKAMURA T., TASHIRO K., NAZAREA M., NAKANO T., SASAYAMA S.,  
RL HOMJO T.; GENOMICS 30:312-319(1995).  
CC -1- FUNCTION: RECEPTOR FOR THE LYMPHOTOXIN-BETA. POSSIBLE FUNCTION IN  
CC IMMUNE DEVELOPMENT.  
CC CC -1- SUBCELLULAR LOCATION: TYPE I MEMBRANE PROTEIN.  
CC DR EMBL; U29173; G681621; -.  
DR EMBL; L38423; G600223; -.  
RW EMBL; U30798; G1061327; -.  
KW RECEPTOR; TRANSMEMBRANE; GLYCOPROTEIN; REPEAT; SIGNAL;  
FT FT SIGNAL 1 30 POTENTIAL.  
FT CHAIN 31 415 LYMPHOTOXIN-BETA RECEPTOR.  
FT DOMAIN 31 223 EXTRACELLULAR (POTENTIAL).  
FT TRANSMEM 224 244 CYTOPLASMIC (POTENTIAL).  
FT DOMAIN 245 415 4 X TNFR-CYS.  
FT REPEAT 42 81 TNFR-CYS 1.  
FT REPEAT 82 124 TNFR-CYS 2.  
FT REPEAT 125 170 TNFR-CYS 3.  
FT REPEAT 171 213 TNFR-CYS 4.  
FT DISULFID 43 58 BY SIMILARITY.  
FT DISULFID 59 72 BY SIMILARITY.  
FT DISULFID 62 80 BY SIMILARITY.  
FT DISULFID 83 98 BY SIMILARITY.  
FT DISULFID 101 116 BY SIMILARITY.  
FT DISULFID 104 124 BY SIMILARITY.  
FT DISULFID 126 132 BY SIMILARITY.  
FT DISULFID 139 150 BY SIMILARITY.  
FT DISULFID 142 169 BY SIMILARITY.  
FT DISULFID 172 187 BY SIMILARITY.  
FT CARBOHYD 40 40 POTENTIAL.  
FT CARBOHYD 179 179 POTENTIAL.  
SQ SEQUENCE 415 AA; 44956 MW; 3C5DD121 CRC32;
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Query Match 9.5%; Score 183; DB 9; Length 415;
Best Local Similarity 35.5%; Pred. No. 8,48e-14;
Matches 33; Conservative 17; Mismatches 33; Indels 10; Gaps 6

Dc 53 pmhdvccrppgpfefavcsrsqdvtkctophnsynehmhlstcqjrcpdvlvgfee 112
::| | |||| : : ::| | |||| : ||:|| | |
Qy 23 SLQDPG-SNCRAG--TF--CDNNRNGISPCPPNFSSAGQG-RTCDICRCRGKV--FRT 74

113 vaptsdtkkaecrqpgmscvylidhecchsee 145
:| :||||| |:| | |||:
Qy 75 RKECSTSNACEDCETPGFHG--LGAGSCMCEOD 105

RESULT 7 STANDARD: PRT: 349 AA.

AC P34015;
DT 01-FEB-1994 (REL. 28, CREATED)
DI 01-FEB-1994 (REL. 28, LAST SEQUENCE UPDATE)
DE 01-JUN-1994 (REL. 29, LAST ANNOTATION UPDATE)
DE PROTEIN C22/B28 HOMOLOG.
GN GAR.
OS VARIOLOA VIRUS.
OC VIIRIDE; DS-DNA ENVELOPED VIRUSES; POXYVIRDAE; CHORDOPOXYVIRINAЕ;
OC ORTHOROXYVIRUSES.
CN [1]

RK STRAIN-INDIA-1967 / ISOLATE IND3;
RM MEDLINE; 93202281.
RA SCHELEJKOVY S.N., BLINOV V.M., SANDAKHCHEV L.S.;
RL FEES LETT. 319:80-83(1993).
CC -1- SIMILARITY: CONTAINS TWO LA-NGR/TNFR-TYPE CYSTEINE-RICH REGIONS.
CW EMBL; X69198; G457087; .-

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DR EMBL: X71177. G516449; -.  
DR PIR: D36858; D36858.  
DR PIR: S35987; S35987.  
DR PIR: S46888; S46888.  
DR HSSP: P19438; 1TNR.  
DR PROSITE: PS00652; TNFR_NGFR.  
KW REPEAT.  
FT DOMAIN 31 108 2 X TNFR-CYS.  
FT REPEAT 31 66 TNFR-CYS 1.  
FT REPEAT 67 108 TNFR-CYS 2.  
SQ SEQUENCE 349 AA; 38189 MW; 50DDB435 CRC32;  
  
Query Match 9.3%; Score 179; DB 10; Length 349;  
Best Local Similarity 34.1%; Pred. No. 3,92e-13;  
Matches 29; Conservative 20; Mismatches 29; Indels 7; Gaps 4;  
  
Db 44 ciscpgtyaarlcstkntgctpcsgqftsrnhlpaciscngnsqvetscnt 103  
|::||: ||: |::||: |:: |:: |:: |:  
QY 28 CINCAGAGF----CDNNNOJCSPCPNPSFSACGQ-RITCDICR-QCKGVFRTRKECSST 81  
|::||: ||: |::||: ||: |::||: |:  
Db 104 hnricecspgyycilkgsag-kac 127  
|::||: ||: |::||: ||: |::||: |:  
QY 82 SNAECDCTFGFHCIGAGCSCMCEQC 106  
|::||: ||: |::||: ||: |::||: |:  
  
RESULT 8  
ID VT2-SFYKA STANDARD; PRT; 325 AA.  
AC P25943;  
DT 01-MAY-1992 (REL. 22, CREATED)  
DI 01-MAY-1992 (REL. 22, LAST SEQUENCE UPDATE)  
DT 01-FEB-1994 (REL. 28, LAST ANNOTATION UPDATE)  
DE TUMOR NECROSIS FACTOR SOLUBLE RECEPTOR PRECURSOR (PROTEIN T2).  
GN T2.  
OS SHOPE FIBROMA VIRUS (STRAIN KASZA) (SFV).  
OC VIRIDAE: DS-DNA ENVELOPED VIRUSES; POXYTRIDAE; CHORDOPOXVIRINE;  
CC LEPORIPOVIRUSES.  
RN [1]  
RP SEQUENCE FROM N.A.  
RX MEDLINE; 87321103.  
RA UPTON C., DELANGE A.M.; MCFADDEN G.;  
RL VIROLOGY 160:20-30(1987).  
RN [2]  
RP FUNCTION.  
RX MEDLINE; 91207415.  
RA SMITH C.A., DAVIS T., WIGNALL J.M., DIN W.S., FARARAH T., UPTON C.,  
RA MCFADDEN G., GOODWIN R.G.;  
RL BIOCHEM. BIOPHYS. RES. COMMUN. 176:335-342(1991).  
CC -I- FUNCTION: BINDS TO TNF-ALPHA AND BETA. PROBABLY PREVENTS TNF TO  
REACH CELLULAR TARGET AND THEREBY DEAMPENING THE POTENTIAL  
ANTIVIRAL EFFECTS OF THE CYTOKINE.  
CC -I- SIMILARITY: CONTAINS A LA-NGFR/TNFR-TYPE CYSTEINE-RICH REGION.  
DR EMBL: M17433; -. NOT_ANNOTATED_CDS.  
DR EMBL: A23727; E199408; -.  
DR PIR: B43692; B43692.  
DR HSSP: P19438; 1TNR.  
DR PROSITE: PS00652; TNFR_NGFR.  
KW RECEPTOR; GLYCOPROTEIN; REPEAT; SIGNAL.  
FT SIGNAL 1 16 POTENTIAL.  
FT CHAIN 17 325 PROTEIN T2.  
FT DOMAIN 27 186 4 X TNFR-CYS.  
FT REPEAT 27 62 TNFR-CYS 1.  
FT REPEAT 63 104 TNFR-CYS 2.  
FT REPEAT 105 147 TNFR-CYS 3.  
FT REPEAT 148 186 TNFR-CYS 4.  
FT CARBOHYD 105 105 POTENTIAL.  
FT CARBOHYD 181 181 POTENTIAL.  
FT CARBOHYD 205 205 POTENTIAL.  
FT CARBOHYD 238 238 POTENTIAL.  
SQ SEQUENCE 325 AA; 35132 MW; C9DDC87B CRC32;
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ID	CD40.MOUSE	STANDARD;	PRT;	289 AA.
AC	P27512;			
DT	01-AUG-1992 (REL. 23, CREATED)			
DT	01-OCT-1996 (REL. 34, LAST SEQUENCE UPDATE)			
DT	01-OCT-1996 (REL. 34, LAST ANNOTATION UPDATE)			
DE	CD40L RECEPTOR PRECURSOR (B-CELL SURFACE ANTIGEN CD40) (BP50) (CDM40)			
GN	CD40L			
OS	MUS MUSCULUS (MOUSE).			
OC	EUCHARYOTA; METAZOA; CHORDATA; VERTEBRATA; TETRAPODA; MAMMALIA;			
OC	BACTERIA; RODENTIA.			
RN	[1]			
RP	SEQUENCE FROM N.A.			
RX	MEDLINE: 92105763.			
RA	TORRES R.M., CLARK E.A.;			
RL	J. IMMUNOL. 148:620-626(1992).			
RN	[2]			
RP	REVISIONS.			
RC	STRAIN-BALB/C;			
RA	TORRES R.M.;			
RL	SUBMITTED (SEP-1996) TO EMBL/GENBANK/DBJ DATA BANKS.			
RN	[3]			
RP	SEQUENCE FROM N.A.			
RC	STRAIN-BALB/C; TISSUE=LIVER;			
RX	MEDLINE: 93094586.			
RA	GRIMAUDI J.C., TORRES R., KOZAK C.A., CHANG R., CLARK E.A.,			
RA	HWARD M., COCKAINE D.A.;			
RL	J. IMMUNOL. 149:3921-3926(1992).			
CC	-1- FUNCTION: RECEPTOR FOR A CYTOKINE LIGAND KNOWN AS CD40L.			
CC	-1- SUBCELLULAR LOCATION: TYPE I MEMBRANE PROTEIN.			
CC	-1- SIMILARITY: CONTAINS A LA-NFIF/TNFR-TYPE CYSTEINE-RICH REGION.			
DR	EMBL; M83121; G1553059; -.			
DR	EMBL; M94126; G192526; -.			
DR	EMBL; M94129; G192526; JOINED.			
DR	EMBL; M94128; G192526; JOINED.			
DR	EMBL; M94127; G192526; JOINED.			
DR	PIR: A46476; A46476.			
DR	HSSP; P19438; TNFR.			
DT	PROSITE; PS00562; TNFR-NGFR.			
DT	RECEPTOR; B-CELL; GLYCOPROTEIN; TRANSMEMBRANE; REPEAT; SIGNAL.			
FT	SIGNAL	1	289	
FT	CHAIN	20	193	
FT	DOMAIN	20	193	
FT	TRANSLEM	194	215	
FT	DOMAIN	216	289	
FT	REPEAT	25	187	
FT	REPEAT	25	187	
FT	REPEAT	61	103	
FT	REPEAT	104	144	
FT	REPEAT	145	187	
FT	REPEAT	153	153	
FT	CARBOHYD	289 AA;	32111 MW;	DBD70A2C CRC32;
FT	SEQUENCE			

Query Match	8.98;	Score 171;	DB 2;	Length 289;
Best Local Similarity	31.28;	Pred. No. 8.18e-12;		
Matches	43;	Conservative 21;	Mismatches 58;	Indels 16;
			Gaps 11;	

Db 51 ctaletky-chnpedsgefsagwreirchqhnrhcepnqglrvkkgtaesdvtctckge 109
 37 CDN-NRNGICSPCPNPNSSA-GGQRNCIDICRQCK-G-VFRTRECSSTSNABDCPPGF 92
 Db 110 hotskdeacacqghpcipgfigmmatatldtvchnpvygfifnqsslfekcypwtsced 169

QY	93	HCLGAGSCMEQD--CKQG---QEL-T-KRG--CKDCFCFTENDQRK--GICRPTNCSL 141
Db	170	knlewlqkqtsqtnvicg 187
		: : : : :
QY	142	DGKSYLVNGTKERDVCG 159

RESULT	10	STANDARD;	PRT;	271 AA.
ID	OX40_RAT			
AC	P15725;			
DT	01-APR-1990 (REL. 14, CREATED)			
DT	01-APR-1990 (REL. 14, LAST SEQUENCE UPDATE)			
DT	01-OCT-1996 (REL. 34, LAST ANNOTATION UPDATE)			
DE	OX40L RECEPTOR PRECURSOR (OX40 ANTIGEN) (MRC OX40).			
GN	TXBP1L OR OX40.			
OS	RATU5 NORVEGICUS (RAT).			
OC	EURAROTLA; METAOLA; CHORDATA; VERTEBRATA; TETRAPODA; MAMMALIA;			
CC	EUTHERIA; RODENTIA.			
RN	[1]			
RP	SEQUENCE FROM N.A.			
RC	TISSUE-T-CELL;			
RX	MEDLINE; 90214614.			
RA	MALLETT S., FOSSUM S., BARCLAY A.N.;			
RL	EMBO J. 9:1063-1068(1990).			
CC	-I- FUNCTION: RECEPTOR FOR THE OX40L/GP34 CYTOKINE.			
CC	-I- SUBCELLULAR LOCATION: TYPE I MEMBRANE PROTEIN.			
CC	-I- TISSUE SPECIFICITY: ACTIVATED T-CELLS.			
CC	-I- SIMILARITY: CONTAINS A IA-NGFR/TNFR-TYPE CYSTEINE-RICH REGION.			
DR	EMBL; X17037; G57831. "			
DR	PIR; S08036; S08036.			
DR	PIR; S12783; S12783.			
DR	PROSITE; PS00652; TNFR_NGFR.			
KW	RECEPTOR; T-CELL; ANTIGEN; GLYCOPROTEIN; TRANSMEMBRANE; REPEAT;			
KW	SIGNAL.			
FT	SIGNAL	1	19	POTENTIAL.
FT	CHAIN	20	271	OX40L RECEPTOR.
FT	DOMAIN	20	210	EXTRACELLULAR (POTENTIAL).
FT	TRANSEM	211	235	POTENTIAL.
FT	DOMAIN	236	271	CYTOPLASMIC (POTENTIAL).
FT	DOMAIN	25	164	4 X TNFR-CYS.
FT	REPEAT	25	60	TNFR-CYS 1.
FT	REPEAT	61	102	TNFR-CYS 2.
FT	REPEAT	103	123	TNFR-CYS 3 (INCOMPLETE).
FT	REPEAT	124	164	TNFR-CYS 4.
FT	CARBOHYD	143	143	POTENTIAL.
SO	SEQUENCE	271 AA;	29895 MM;	65460ED2 CRC32;

Query Match	8.6%;	Score 166;	DB 7;	Length 271;
Best Local Similarity	30.6%;	Pred. No. 5.33e-11;		
Matches	38;	Conservative	25;	Mismatches 48;
				Indels 13;
				Gaps 5;

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Db 51 cdhrtdvchpceegfyneayntqkqcgqcmhrrsselkqncotpedtvcvcrqgtq- 109
   || : : : : : : : : : : : : : : : : : : : : : : : : : : : :
QY 37 cdnrrnqtcscfprnssrssaagqrtdicrnc-kgvfrtrkecsstsnacdcotpefhc 94
   || : : : : : : : : : : : : : : : : : : : : : : : : : : : :
Db 110 ----pr--gds--shklgv-dcvpcepghfsgpsnackpwtnctlsqkqlhpnasnl 159
   || : : : : : : : : : : : : : : : : : : : : : : : : : : : :
QY 95 lgaagsmcqcdkqogeltkrgkdcfcgffndokrgicrprwtncslsdgksvlangfker 154
   || : : : : : : : : : : : : : : : : : : : : : : : : : : : :
Db 160 dtvc 163
   || : : : : : : : : : : : : : : : : : : : : : : : : : : : :
QY 155 dvvc 158
   || : : : : : : : : : : : : : : : : : : : : : : : : : : : :

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ESULT	11	STANDARD:	PRT:	435	AA.
D	TNRC_HUMAN				

AC
01-JUN-1994 (REL. 29, CREATED)
DT
01-JUN-1994 (REL. 29, LAST SEQUENCE UPDATE)
DT
01-OCT-1996 (REL. 34, LAST ANNOTATION UPDATE)
DE
LYMPHOTOXIN-BETA RECEPTOR PRECURSOR (TUMOR NECROSIS FACTOR RECEPTOR
DE
2 RELATED PROTEIN) (TUMOR NECROSIS FACTOR C RECEPTOR).
GN
TNFR.

OS HOMO SAPIENS (HUMAN).
 OC EUKARYOTA; METAZOA; CHORDATA; VERTEBRATA; TETRAPODA; MAMMALIA;
 OC EUTHERIA; PRIMATES.
 RN [1]
 RP SEQUENCE FROM N.A.
 RC TISSUE=LIVER;
 RX MEDLINE: 93252381.
 RA BAENS M., CHAFANET M., CASSIMAN J.J., DEN BERGHE H., MARINEN P.,
 RL CLASSENS E., NOELLE R.J., FELL H.;
 RN J. IMMUNOL. 151:5261-5271(1993).
 RP [2]
 RP FUNCTION;
 RX MEDLINE: 94225209.
 RA CROME P.D., VAN ARSDALE T.L., WALTER B.N., WARE C.F., HESSON C.,
 RH EREFFER B., BROWNING J.L., DIN W.S., GOODWIN R.G., SMITH C.A.;
 RL SCIENCE 264:707-710(1994).
 CC -1- FUNCTION: RECEPTOR FOR THE LYMPHOTOXIN-BETA. POSSIBLE FUNCTION IN
 CC IMMUNE DEVELOPMENT.
 CC -1- SUBCELLULAR LOCATION: TYPE I MEMBRANE PROTEIN.
 CC -1- SIMILARITY: CONTAINS A LA-NGFR/TNFR-TYPE CYSTEINE-RICH REGION.
 DR EMBL: L04270; G339762; -.
 DR EMBL: 600979; -.
 DR EMBL: P19999; 1CLG.
 FT PROSITE: PS00652; TNFR_NGFR.
 KW RECEPTOR; TRANSMEMBRANE; GLYCOPROTEIN; REPEAT; SIGNAL.
 FT SIGNAL 1 30
 FT CHAIN 31 435
 FT DOMAIN 31 227
 FT TRANSMEM 228 248
 FT DOMAIN 249 435
 FT DOMAIN 42 211
 FT REPEAT 42 81
 FT REPEAT 82 124
 FT REPEAT 125 168
 FT REPEAT 169 211
 FT REPEAT 211 211
 FT DISULFID 43 58
 FT DISULFID 59 72
 FT DISULFID 62 80
 FT DISULFID 83 98
 FT DISULFID 101 116
 FT DISULFID 104 124
 FT DISULFID 126 132
 FT DISULFID 139 148
 FT DISULFID 142 167
 FT DISULFID 170 185
 FT CARBOHYD 40 40
 FT CARBOHYD 177 177
 SQ SEQUENCE 435 AA; 46709 MW; 203882DD CRC32;
 Query Match 8.2%; Score 158; DB 9; Length 435;
 Best Local Similarity 31.5%; Pred. No. 1.03e-09;
 Matches 52; Conservative 26; Mismatches 66; Indels 21; Gaps 13;
 Db 59 csrccpptyvskscrlrdtvcatacaensynehmyltlclqclrcpypmgleiapcts 118
 Qy 28 CSNCPAGTF---CDNNRNQICSPCPNFSFA-GGORTDIDRCCKGV--FTRKRCSS 80
 Db 119 krttgcrcqpmcaawalectccllscdpgtcaelkdevkqnmhcyrcakghfnt 178
 Qy 81 TSAEEDCPPEFHCLG-A-GCSMCE--QDCKQG-Q-ELTK--KGCKDC--C-FGTF-ND 127
 Db 179 ssparscphtcengglveaapgtasdtclknplelpmmsg 223
 Qy 128 QKRGT-CRPWTNCSLDGKSVLVNGTKRDVYCGPSPADLSFGASS 171
 RESULT 12
 ID OX40_MOUSE STANDARD; PRT; 272 AA.
 AC P47741;
 DT 01-FEB-1996 (REL. 33, CREATED)
 DT 01-FEB-1996 (REL. 33, LAST SEQUENCE UPDATE)
 DT 01-OCT-1996 (REL. 34, LAST ANNOTATION UPDATE)
 DE OX40L RECEPTOR PRECURSOR (OX40 ANTIGEN).
 GN TXGP1L OR OX40.

OS MUS MUSCULUS (MOUSE).
 OC EUKARYOTA; METAZOA; CHORDATA; VERTEBRATA; TETRAPODA; MAMMALIA;
 OC EUTHERIA; RODENTIA.
 RN [1]
 RP SEQUENCE FROM N.A.
 RC STRAIN=BALE/C;
 RX MEDLINE: 94044750.
 RA CALDERHEAD D.M., BUHLMANN J.E., VAN DEN EERTWEGH A.J.,
 RL CLASSENS E., NOELLE R.J., FELL H.;
 RN J. IMMUNOL. 151:5261-5271(1993).
 RP [2]
 RP SEQUENCE FROM N.A.
 RX MEDLINE: 95255413.
 RA BIRKELAND M.L., COPELAND N.G., GILBERT D.J., JENKINS N.A.,
 RL BARCLAY A.N.;
 RL EUR. J. IMMUNOL. 25:926-930(1995).
 CC -1- FUNCTION: RECEPTOR FOR THE OX40L/GP34 CYTOKINE.
 CC -1- SUBCELLULAR LOCATION: TYPE I MEMBRANE PROTEIN.
 CC -1- SIMILARITY: CONTAINS A LA-NGFR/TNFR-TYPE CYSTEINE-RICH REGION.
 DR EMBL: 221674; G312828; -.
 DR EMBL: X85214; G332819; -.
 KW RECEPTOR; T-CELL; ANTIGEN; GLYCOPROTEIN; TRANSMEMBRANE; REPEAT;
 FT SIGNAL 1 19
 FT CHAIN 20 272
 FT DOMAIN 20 211
 FT TRANSMEM 212 236
 FT DOMAIN 237 272
 FT DOMAIN 26 165
 FT REPEAT 26 61
 FT REPEAT 62 103
 FT REPEAT 104 124
 FT REPEAT 125 165
 FT CARBOHYD 144 144
 FT CARBOHYD 15 15
 SQ SEQUENCE 272 AA; 30153 MW; 67D1B978 CRC32;
 Query Match 7.3%; Score 140; DB 7; Length 272;
 Best Local Similarity 30.6%; Pred. No. 6.53e-07;
 Matches 38; Conservative 21; Mismatches 52; Indels 13; Gaps 5;
 Db 52 cdhttrdtlhcpeetfyneavnydtckgctgcghrsagselkngcuptgtvrcrpgtg- 110
 Qy 37 CDNNRNQICSPCPNFSFSSAGGORTDIDRCG-KGVFTRKRCSS TSAEEDCPPEFHCLG 94
 Db 111 -----pr--qds--gyklgv-dcvpcpghsfspgnnqackpwtncltsgktrhpsdsi 160
 Qy 95 LGAGCSMCQDCKQGGELTKKGCDCCFSTFNDKRGICRPWTNCSLDGKSVLVNGTKER 154
 Db 161 dvvc 164
 Qy 155 DVVC 158
 RESULT 13
 ID OX40_HUMAN STANDARD; PRT; 277 AA.
 AC P43489;
 DT 01-NOV-1995 (REL. 32, CREATED)
 DT 01-NOV-1995 (REL. 32, LAST SEQUENCE UPDATE)
 DT 01-FEB-1996 (REL. 33, LAST ANNOTATION UPDATE)
 DE OX40L RECEPTOR PRECURSOR (ACT35 ANTIGEN) (TXA-TRANSCRIPTIONALLY
 DE ACTIVATED GLYCOPROTEIN 1 RECEPTOR).
 GN TXGP1L.
 OS HOMO SAPIENS (HUMAN).
 OC EUKARYOTA; METAZOA; CHORDATA; VERTEBRATA; TETRAPODA; MAMMALIA;
 OC EUTHERIA; PRIMATES.
 RN [1]
 RP SEQUENCE FROM N.A.
 RX MEDLINE: 94170844.
 RA LATZA U., DUERKOP H., SCHNITZER S., RINGELING J., EITELBACH F.,
 RA HUMMEL M., FORATSCHE C., STEIN H.;
 RL EUR. J. IMMUNOL. 24:677-683(1994).
 CC -1- FUNCTION: RECEPTOR FOR THE OX40L/GP34 CYTOKINE.

FT	DOMAIN	216	277	CYTOPLASMIC (POTENTIAL).
FT	DOMAIN	25	187	4 X TNFR-CYS.
FT	REPEAT	25	60	TNFR-CYS 1.
FT	REPEAT	61	103	TNFR-CYS 2.
FT	REPEAT	104	144	TNFR-CYS 3.
FT	REPEAT	145	187	TNFR-CYS 4.
FT	CARBOHYD	153	153	POTENTIAL.
FT	CARBOHYD	180	180	POTENTIAL.
SO	SEQUENCE	277 AA:	30619 MM:	3B284411 CRC32;

Query Match 7.1%; Score 136; DB 2; Length 277;
 Best Local Similarity 28.3%; Pred. No. 2.63e-06;
 Matches 39; Conservative 24; Mismatches 61; Indels 14; Gaps 10;

Db	51	ctetctecclpcgeselfldwrethchqkycdpnlglyvqgkgtsetdlctceegwh	110
QY	37	CDNNRNQICSPCPNPSFSSAGGRT-CDICRQK-GV-FRTKKECSSTSMNECDCTPGEH	93
Db	111	ctseacescvlhrcspgfygkqiatgvsdtlcepcpygffsnvsafekchpytscetk	170
QY	94	CLGAGCSMCE-Q-DCKQGQELTK--KGCKD--C--C-FGTINDQKRGI--CRPWTCSLD	142
Db	171	dlvvqgagtnktdvvcgp	188
QY	143	GKSYLVNGTKERDYYVCGP	160

Search completed: Tue Mar 24 17:04:31 1998
 Job time : 48 secs.